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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2          "Ask CAS" for self-help around the clock
 NEWS  3  SEP 09  CA/CAplus records now contain indexing from 1907 to the
                  present
 NEWS  4  DEC 08  INPADOC: Legal Status data reloaded
 NEWS  5  SEP 29  DISSABS now available on STN
 NEWS  6  OCT 10  PCTFULL: Two new display fields added
 NEWS  7  OCT 21  BIOSIS file reloaded and enhanced
 NEWS  8  OCT 28  BIOSIS file segment of TOXCENTER reloaded and enhanced
 NEWS  9  NOV 24  MSDS-CCOHS file reloaded
 NEWS 10  DEC 08  CABA reloaded with left truncation
 NEWS 11  DEC 08  IMS file names changed
 NEWS 12  DEC 09  Experimental property data collected by CAS now available
                  in REGISTRY
 NEWS 13  DEC 09  STN Entry Date available for display in REGISTRY and CA/CAplus
 NEWS 14  DEC 17  DGENE: Two new display fields added
 NEWS 15  DEC 18  BIOTECHNO no longer updated
 NEWS 16  DEC 19  CROPU no longer updated; subscriber discount no longer
                  available
 NEWS 17  DEC 22  Additional INPI reactions and pre-1907 documents added to CAS
                  databases
 NEWS 18  DEC 22  IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22  ABI-INFORM now available on STN
 NEWS 20  JAN 27  Source of Registration (SR) information in REGISTRY updated
                  and searchable
 NEWS 21  JAN 27  A new search aid, the Company Name Thesaurus, available in
                  CA/CAplus
 NEWS 22  FEB 05  German (DE) application and patent publication number format
                  changes
 NEWS 23  MAR 03  MEDLINE and LMEDLINE reloaded
 NEWS 24  MAR 03  MEDLINE file segment of TOXCENTER reloaded
 NEWS 25  MAR 03  FRANCEPAT now available on STN
 NEWS 26  MAR 29  Pharmaceutical Substances (PS) now available on STN
 NEWS 27  MAR 29  WPIFV now available on STN
 NEWS 28  MAR 29  No connect hour charges in WPIFV until May 1, 2004
 NEWS 29  MAR 29  New monthly current-awareness alert (SDI) frequency in RAPRA

 NEWS EXPRESS  MARCH 5 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 3 MARCH 2004
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FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004

=> file medline, uspatful, dgene, embase, wpids, fsta, cen, biosis,
COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION

FULL ESTIMATED COST 0.21 0.21

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=> s FRT or FLP
L2 6180 FRT OR FLP

=> s cre lox
L3 1238 CRE LOX

=> s l2 and stable recombination
L4 0 L2 AND STABLE RECOMBINATION

=> s FRT () FLP
L5 96 FRT (W) FLP

=> s l5 and recombination
L6 82 L5 AND RECOMBINATION

=> s l6 and stability
L7 27 L6 AND STABILITY

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L7 ANSWER 1 OF 27 MEDLINE on STN
TI High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2 microns plasmid system.
AB The best candidate for a high-copy-number and mitotic **stability** expression system in yeast is the endogenous 2 microns plasmid. Nevertheless, derivatives of the 2 microns plasmid typically exhibit lower copy numbers and require selection for adequate maintenance within cells. We report the construction and utilization of an efficient heterologous gene expression system containing a 4.5-kb inducible expression cassette inserted into the 2 microns plasmid and selected in cells utilizing a carrier plasmid which is subsequently lost via **FRT/Flp recombination**. The non-selectable 2 micron plasmid, containing the cassette, was found to be stably maintained in cells, without selection, at high copy number. The dynamics of resolution and partitioning of this plasmid were analyzed during the course of 50 generations of growth under non-selective conditions. The heterologous lacZ reporter gene coding for beta-galactosidase (beta Gal) is driven by the hybrid, galactose-inducible promoter GAL10::pMF alpha 1. Upon induction, beta Gal was secreted into the periplasm and culture supernatant at levels which could be detected directly from Coomassie blue-stained SDS-PAGE. Furthermore, plasmid-containing cells could be maintained directly on rich YPD medium and identified either by utilizing XGal or by observing inhibition of colony growth on YPGal solid medium. The cassette was designed for direct, high-level, inducible expression of cloned genes downstream from the MF alpha 1 signal sequence, with or without a C-terminal lacZ fusion. This vector represents the first demonstration of a non-selectable, mitotically stable, episomal plasmid system capable of expressing recombinant proteins at high levels.(ABSTRACT TRUNCATED AT 250 WORDS)
ACCESSION NUMBER: 94010342 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8406040
TITLE: High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2 microns plasmid system.
AUTHOR: Ludwig D L; Ugolini S; Bruschi C V
CORPORATE SOURCE: Microbiology Department, International Centre for Genetic Engineering and Biotechnology, Trieste, Italy.
SOURCE: Gene, (1993 Sep 30) 132 (1) 33-40.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199311
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931119

L7 ANSWER 2 OF 27 USPATFULL on STN
TI Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes
AB The invention provides methods for generating, identifying, and selecting polynucleotides encoding novel starch metabolizing enzymes (NSME), NSME-encoding polynucleotides, compositions of recombinant shuffled NSME protein, plant cells and microbes containing a shuffled NSME polynucleotide in expressible form, plants containing a shuffled NSME polynucleotide in expressible form, novel starch compositions produced by plants and cells, uses of such plants, cells, and starch compositions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2004:59856 USPATFULL
TITLE:	Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes
INVENTOR(S):	Stemmer, Willem P. C., Los Gatos, CA, United States Subramanian, Venkitswaran, San Diego, CA, United States Raillard, Sun Ai, Mountain View, CA, United States Huisman, Gjalt, San Carlos, CA, United States
PATENT ASSIGNEE(S):	Maxygar, Inc., Redwood City, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6703240	B1	20040309	
APPLICATION INFO.:	US 2000-547844		20000412	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-129009P	19990413 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	GRANTED
PRIMARY EXAMINER:	Reynolds, Deborah J.
ASSISTANT EXAMINER:	Woitach, Joseph
LEGAL REPRESENTATIVE:	Holmer, Christopher, Kruse, Norman J., Townsend & Townsend & Crew
NUMBER OF CLAIMS:	82
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	3 Drawing Figure(s); 3 Drawing Page(s)
LINE COUNT:	2972

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 27 USPATFULL on STN

TI In vitro mutagenesis, phenotyping, and gene mapping

AB Cellular libraries useful for in vitro phenotyping and gene mapping. In a representative approach, a method for preparing a homozygous cellular library includes the steps of providing a heterozygous cellular library comprising a plurality of isolated parent cells; inducing site-specific mitotic **recombination** in the plurality of isolated parent cells; culturing the plurality of isolated parent cells, whereby a population of daughter cells is produced; and selecting daughter cells comprising a homozygous genetic modification, whereby a homozygous cellular library is prepared.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2004:44603 USPATFULL
TITLE:	In vitro mutagenesis, phenotyping, and gene mapping
INVENTOR(S):	Threadgill, David W., Chapel Hill, NC, UNITED STATES Lee, Daekee, Chapel Hill, NC, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2004033596	A1	20040219	
APPLICATION INFO.:	US 2003-428977	A1	20030502	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2002-377864P	20020502 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	JENKINS & WILSON, PA, 3100 TOWER BLVD, SUITE 1400, DURHAM, NC, 27707
NUMBER OF CLAIMS:	71
EXEMPLARY CLAIM:	1

NUMBER OF DRAWINGS: 6 Drawing Page(s)
LINE COUNT: 3125
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 27 USPATFULL on STN
TI Self-rearranging DNA vectors
AB Disclosed are replicatable viral DNA vectors encoding a site-specific DNA-altering enzyme and a DNA target recognized by the enzyme, the enzyme selectively converting, in a cell expressing the enzyme, the DNA vector to a rearranged form. The invention further relates to methods for assembling recombinant adenoviral DNAs. These methods include the steps of: (a) providing a first linearized DNA vector including a restriction site and a cos site and a second linearized DNA vector including the restriction site, an adenoviral nucleic acid molecule, and a cos site; and (b) ligating the first and second linearized DNA vectors, the ligation assembling a recombinant adenoviral DNA.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2004:38117 USPATFULL
TITLE: Self-rearranging DNA vectors
INVENTOR(S): Seed, Brian, Boston, MA, UNITED STATES
Freeman, Mason Wright, Lincoln, MA, UNITED STATES
Kovtun, Alexander, Acton, MA, UNITED STATES
Murakawa, Masahiro, Fukuoka City, JAPAN
Park, Eun-Chung, Washington, DC, UNITED STATES
Wang, Xinzhong, Framingham, MA, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004028653	A1	20040212
APPLICATION INFO.:	US 2003-384136	A1	20030307 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. WO 2001-US27682, filed on 7 Sep 2001, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-246904P	20001108 (60)
	US 2000-231053P	20000908 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: CLARK & ELBING LLP, 101 FEDERAL STREET, BOSTON, MA, 02110
NUMBER OF CLAIMS: 34
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 40 Drawing Page(s)
LINE COUNT: 3577
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 27 USPATFULL on STN
TI Compositions and methods for making mutations in cell lines and animals
AB The present invention is directed generally to reduction or inactivation of gene function or gene expression in cells in vitro and in multicellular organisms. The invention encompasses methods for mutating cells using a combination of mutagens, particularly wherein at least one mutagen is an insertional mutagen, to achieve homozygous gene mutation or mutation of multiple genes required cumulatively to achieve a phenotype to create knock-outs, knock-downs, and other modifications in the same cell. The invention is also directed to cells (and libraries thereof) and organisms created by the methods of the invention, including those in which at least one of the genes created by insertional mutagenesis is tagged by means of the insertion sequences thereby allowing identification of the mutated gene(s). The invention is also directed to libraries of mutated cells and their uses. The invention is also directed to methods of identifying mutations with

methods of the invention, in cells (and libraries thereof) and organisms, by means of the insertional tag.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2004:24785 USPATFULL
TITLE:	Compositions and methods for making mutations in cell lines and animals
INVENTOR(S):	Harrington, John Joseph, Mentor, OH, UNITED STATES Jackson, Paul David, Shaker Heights, OH, UNITED STATES Jiang, Li, Hudson, OH, UNITED STATES
PATENT ASSIGNEE(S):	Athersys, Inc., Cleveland, OH, 44115 (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004018624	A1	20040129
APPLICATION INFO.:	US 2002-277612	A1	20021022 (10)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 2002-196721, filed on 15 Jul 2002, ABANDONED		

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-336497P	20011022 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109
NUMBER OF CLAIMS:	170
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	21 Drawing Page(s)
LINE COUNT:	4151

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 27 USPATFULL on STN

TI Compositions and methods for the targeted insertion of a nucleotide sequence of interest into the genome of a plant

AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2004:3409 USPATFULL
TITLE:	Compositions and methods for the targeted insertion of a nucleotide sequence of interest into the genome of a plant
INVENTOR(S):	Baszczynski, Christopher L., Urbandale, IA, UNITED STATES Bowen, Benjamin A., Berkeley, CA, UNITED STATES Peterson, David J., Ames, IA, UNITED STATES Tagliani, Laura, Zionsville, IN, UNITED STATES
PATENT ASSIGNEE(S):	Pioneer Hi-Bred International, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004003435	A1	20040101
APPLICATION INFO.:	US 2003-440030	A1	20030516 (10)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994		

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC., BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE 4000, CHARLOTTE, NC, 28280-4000
NUMBER OF CLAIMS: 22
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Page(s)
LINE COUNT: 1546
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 7 OF 27 USPATFULL on STN
TI Compositions and methods to reduce the complexity of transgene integration into the genome of a plant
AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:336227 USPATFULL
TITLE: Compositions and methods to reduce the complexity of transgene integration into the genome of a plant
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, UNITED STATES
Bowen, Benjamin A., Berkeley, CA, UNITED STATES
Peterson, David J., Ames, IA, UNITED STATES
Tagliani, Laura, Zionsville, IN, UNITED STATES
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003237107	A1	20031225
APPLICATION INFO.:	US 2003-430908	A1	20030507 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC., BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE 4000, CHARLOTTE, NC, 28280-4000
NUMBER OF CLAIMS: 23
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Page(s)
LINE COUNT: 1556
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 27 USPATFULL on STN
TI Compositions and methods for locating preferred integration sites within

the genome of a plant

AB Methods to find optimal integration sites within a plant genome are provided. More particularly, a plant is transformed with a target site having an expression cassette comprising a nucleotide sequence operably linked to a promoter active in the plant. The target site is flanked by non-identical **recombination** sites. Transformed protoplast, tissues, or whole plants can be tested to determine the levels of activity of the inserted gene. By comparison of cellular activities of the gene in different insertion sites, preferred integration sites may be found wherein the gene is expressed at high or acceptable levels. These plants can then be utilized with subsequent retargeting techniques to replace the nucleotide sequence with other genes or nucleotide sequences of interest contained in a transfer cassette.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:320407 USPATFULL

TITLE: Compositions and methods for locating preferred integration sites within the genome of a plant

INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, UNITED STATES
Bowen, Benjamin A., Berkeley, CA, UNITED STATES
Peterson, David J., Ames, IA, UNITED STATES
Tagliani, Laura, Zionsville, IN, UNITED STATES

PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003226160	A1	20031204
APPLICATION INFO.:	US 2003-430907	A1	20030507 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility

FILE SEGMENT: APPLICATION

LEGAL REPRESENTATIVE: ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC., BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE 4000, CHARLOTTE, NC, 28280-4000

NUMBER OF CLAIMS: 17

EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 2 Drawing Page(s)

LINE COUNT: 1537

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 27 USPATFULL on STN

TI Compositions and methods for making mutations in cell lines and animals

AB The present invention is directed generally to reduction or inactivation of gene function or gene expression in cells in vitro and in multicellular organisms. The invention encompasses methods for mutating cells using a combination of mutagens, particularly wherein at least one mutagen is an insertional mutagen, to achieve homozygous gene mutation or mutation of multiple genes required cumulatively to achieve a phenotype to create knock-outs, knock-downs, and other modifications in the same cell. The invention is also directed to cells (and libraries thereof) and organisms created by the methods of the invention, including those in which at least one of the genes created by insertional mutagenesis is tagged by means of the insertion sequences thereby allowing identification of the mutated gene(s). The invention is also directed to libraries of mutated cells and their uses. The

invention is also directed to methods of identifying mutations with methods of the invention, in cells (and libraries thereof) and organisms, by means of the insertional tag.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:318774 USPATFULL
TITLE:	Compositions and methods for making mutations in cell lines and animals
INVENTOR(S):	Harrington, John Joseph, Mentor, OH, UNITED STATES Jackson, Paul David, Shaker Heights, OH, UNITED STATES Jiang, Li, Hudson, OH, UNITED STATES
PATENT ASSIGNEE(S):	Athersys, Inc., Cleveland, OH (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003224519	A1	20031204
APPLICATION INFO.:	US 2003-345115	A1	20030115 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2002-277612, filed on 22 Oct 2002, PENDING Continuation-in-part of Ser. No. US 2002-196721, filed on 15 Jul 2002, ABANDONED

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-336497P	20011022 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109
NUMBER OF CLAIMS:	210
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	21 Drawing Page(s)
LINE COUNT:	4363

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 27 USPATFULL on STN

TI DNA sequences comprising gene transcription regulatory qualities and methods for detecting and using such DNA sequences

AB The invention is concerned with the systematic elucidation and identification of regulatory sequences. The invention provides among others screenings and detection methods with which regulatory sequences can be identified. The invention further provides regulatory sequences and use thereof in various fields such as, but not limited to protein production, diagnostics, transgenic plants and animals, and the therapeutic field.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:283124 USPATFULL
TITLE:	DNA sequences comprising gene transcription regulatory qualities and methods for detecting and using such DNA sequences
INVENTOR(S):	Otte, Arie Peter, Purmerend, NETHERLANDS Kruckeberg, Arthur Leo, Amsterdam, NETHERLANDS

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003199468	A1	20031023
APPLICATION INFO.:	US 2002-190312	A1	20020705 (10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2001-303199P	20010705 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	TRASK BRITT, P.O. BOX 2550, SALT LAKE CITY, UT, 84110
NUMBER OF CLAIMS:	77

EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 65 Drawing Page(s)
LINE COUNT: 4902
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 27 USPATFULL on STN
TI Compositions for the genetic modification of plants
AB Methods and compositions for the targeted integration of nucleotide sequences into a plant are provided. Particularly, the present invention is drawn to compositions comprising polynucleotide sequences having the following operably linked components: an intron, a nucleotide sequence of interest, and a terminator region, wherein the polynucleotide sequence comprises one or more **recombination** sites. The **recombination** sites are non-identical to one another and one of the **recombination** sites is contained within the intron.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:253688 USPATFULL
TITLE: Compositions for the genetic modification of plants
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States
Bowen, Benjamin A., Des Moines, IA, United States
Peterson, David J., Ames, IA, United States
Tagliani, Laura A., Ankeny, IA, United States
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6624297	B1	20030923
APPLICATION INFO.:	US 1999-455050		19991206 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2001

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Fox, David T.
ASSISTANT EXAMINER: Kruse, David H
LEGAL REPRESENTATIVE: Alston & Bird LLP
NUMBER OF CLAIMS: 15
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 1599
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 27 USPATFULL on STN
TI Compositions and methods to reduce the complexity of transgene integration in the genome of a plant
AB Methods for reducing the complexity of integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:149071 USPATFULL

TITLE: Compositions and methods to reduce the complexity of transgene integration in the genome of a plant
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States
Bowen, Benjamin A., Des Moines, IA, United States
Peterson, David J., Ames, IA, United States
Tagliani, Laura A., Ankeny, IA, United States
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6573425	B1	20030603
APPLICATION INFO.:	US 1999-439042		19991112 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Fox, David T.
ASSISTANT EXAMINER: Kruse, David H
LEGAL REPRESENTATIVE: Alston & Bird LLP
NUMBER OF CLAIMS: 37
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 1650
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 13 OF 27 USPATFULL on STN
TI Universal stem cells
AB The subject invention pertains to materials and methods for preparing multi-potential stem cells having a pre-selected expression of MHC antigens. Stem cells of the subject invention can be used to generate histocompatible tissues/organs for transplantation. The process of the subject invention comprises the use of targeting vectors capable of gene knockout, insertion of site-specific **recombination** cassettes, and the replacement of histocompatibility alleles in the stem cell. Novel knockout vectors are used to delete designated regions of one chromosome. **Recombination** cassette vectors are then used to delete the same region on the second chromosome and deposit a site-specific **recombination** cassette which can be utilized by replacement vectors for inserting the new MHC genes on the chromosome of the engineered cell. The subject invention also pertains to cells, tissues, and transgenic mammal prepared using the methods and materials of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:147717 USPATFULL
TITLE: Universal stem cells
INVENTOR(S): Lawman, Patricia, Chipley, FL, UNITED STATES
Lawman, Michael J.P., Chipley, FL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003101465	A1	20030529
APPLICATION INFO.:	US 2002-186231	A1	20020628 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-47769, filed on 25 Mar 1998, ABANDONED

	NUMBER	DATE

PRIORITY INFORMATION:	US 1997-42358P	19970325 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	APPLICATION	
LEGAL REPRESENTATIVE:	SALIWANCHIK LLOYD & SALIWANCHIK, A PROFESSIONAL ASSOCIATION, 2421 N.W. 41ST STREET, SUITE A-1, GAINESVILLE, FL, 326066669	
NUMBER OF CLAIMS:	18	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	6 Drawing Page(s)	
LINE COUNT:	1852	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 14 OF 27 USPATFULL on STN

TI Compositions and methods for locating preferred integration sites within a plant genome

AB Methods to find optimal integration sites within a plant genome are provided. More particularly, a plant is transformed with a target site having an expression cassette comprising a nucleotide sequence operably linked to a promoter active in the plant. The target site is flanked by non-identical **recombination** sites, Transformed protoplast, tissues, or whole plants can be tested to determine the levels of activity of the inserted gene, By comparison of cellular activities of the gene in different insertion sites, preferred integration sites may be found wherein the gene is expressed at high or acceptable levels. These plants can then be utilized with subsequent retargeting techniques to replace the nucleotide sequence with other genes or nucleotide sequences of interest contained in a transfer cassette.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:109223 USPATFULL		
TITLE:	Compositions and methods for locating preferred integration sites within a plant genome		
INVENTOR(S):	Baszczynski, Christopher L., Urbandale, IA, United States Bowen, Benjamin A., Des Moines, IA, United States Peterson, David J., Ames, IA, United States Tagliani, Laura A., Ankeny, IA, United States		
PATENT ASSIGNEE(S):	Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6552248	B1	20030422
APPLICATION INFO.:	US 1999-438239		19991112 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2001		
	NUMBER		DATE
PRIORITY INFORMATION:	US 1997-65627P		19971118 (60)
	US 1997-65613P		19971118 (60)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	GRANTED		
PRIMARY EXAMINER:	Fox, David T.		
ASSISTANT EXAMINER:	Kruse, David H		
LEGAL REPRESENTATIVE:	Alston & Bird LLP		
NUMBER OF CLAIMS:	49		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	2 Drawing Figure(s); 2 Drawing Page(s)		
LINE COUNT:	1684		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 15 OF 27 USPATFULL on STN
TI Methods for improving a photosynthetic carbon fixation enzyme
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having photosynthetic carbon fixation activities, including Rubisco and Rubisco activase activities, which are useful for introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2003:106224 USPATFULL		
TITLE:	Methods for improving a photosynthetic carbon fixation enzyme		
INVENTOR(S):	Zhu, Genhai, San Jose, CA, UNITED STATES		
PATENT ASSIGNEE(S):	Maxygen, Inc. (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003073135	A1	20030417
APPLICATION INFO.:	US 2002-271019	A1	20021015 (10)
	NUMBER		DATE
PRIORITY INFORMATION:	US 2001-328871P		20011012 (60)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	MAXYGEN, INC., INTELLECTUAL PROPERTY DEPARTMENT, 515 GALVESTON DRIVE, RED WOOD CITY, CA, 94063		
NUMBER OF CLAIMS:	20		
EXEMPLARY CLAIM:	1		
LINE COUNT:	2569		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 16 OF 27 USPATFULL on STN
TI Modified ADP-glucose pyrophosphorylase for improvement and optimization of plant phenotypes
AB The invention provides methods and compositions relating to sequence-shuffled variants of ADP-glucose pyrophosphorylase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:304117 USPATFULL		
TITLE:	Modified ADP-glucose pyrophosphorylase for improvement and optimization of plant phenotypes		
INVENTOR(S):	Stemmer, Willem P. C., Los Gatos, CA, United States Subramanian, Venkiteswaran, San Diego, CA, United States		
PATENT ASSIGNEE(S):	Maxygen, Inc., Redwood City, CA, United States (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6483011	B1	20021119
APPLICATION INFO.:	US 2000-721540		20001122 (9)
RELATED APPLN. INFO.:	Continuation of Ser. No. US 1999-437725, filed on 9 Nov 1999, now abandoned		
	NUMBER		DATE
PRIORITY INFORMATION:	US 1998-107782P		19981110 (60)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	GRANTED		
PRIMARY EXAMINER:	Horlick, Kenneth R.		
ASSISTANT EXAMINER:	Strzelecka, Teresa		
LEGAL REPRESENTATIVE:	Townsend and Townsend and Crew LLP		

NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 2975
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 17 OF 27 USPATFULL on STN
TI Alpha-tocopherol transfer protein knockout animals
AB This invention provides knockout animals comprising a disruption in one or both alleles of the gene encoding alpha-tocopherol transfer protein (TTP). The knockout animals provide good model systems for atherosclerosis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:302526 USPATFULL
TITLE: Alpha-tocopherol transfer protein knockout animals
INVENTOR(S): Farese, Robert V., JR., San Francisco, CA, UNITED STATES
Terasawa, Yuko, Campbell, CA, UNITED STATES
Traber, Maret G., Corvallis, OR, UNITED STATES
PATENT ASSIGNEE(S): The Regents of the University of California (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002170080	A1	20021114	
APPLICATION INFO.:	US 2001-1278	A1	20011101	(10)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-245302P	20001102 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: QUINE INTELLECTUAL PROPERTY LAW GROUP, P.C., P O BOX 458, ALAMEDA, CA, 94501
NUMBER OF CLAIMS: 56
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 4 Drawing Page(s)
LINE COUNT: 1912
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 18 OF 27 USPATFULL on STN
TI METHODS FOR OBTAINING A POLYNECLEOTIDE ENCODING A POLYPEPTIDE HAVING A RUBISCO ACTIVITY
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having Rubisco biosynthetic enzyme activities which are useful for introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:272896 USPATFULL
TITLE: METHODS FOR OBTAINING A POLYNECLEOTIDE ENCODING A POLYPEPTIDE HAVING A RUBISCO ACTIVITY
INVENTOR(S): STEMMER, WILLEM P. C., LOS GATOS, CA, UNITED STATES
SUBRAMANIAN, VENKITSWARAN, SAN DIEGO, CA, UNITED STATES
ZHU, GENHAI, SUNNYVALE, CA, UNITED STATES
LIU, LU, REDWOOD CITY, CA, UNITED STATES
SELIFONOV, SERGEY A., LOS ALTOS, CA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002151017	A1	20021017	
APPLICATION INFO.:	US 1999-437726	A1	19991109	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-153093P	19990909 (60)
	US 1998-107756P	19981110 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834
NUMBER OF CLAIMS: 26
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 3434
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 19 OF 27 USPATFULL on STN
TI Compositions and methods for the targeted removal of a nucleotide sequence from the genome of a plant
AB Methods and compositions to remove a nucleotide sequence of interest in a plant and plant cell are provided. In particular the methods of the invention comprise providing a plant cell having stably incorporated into its genome a transfer cassette comprising a nucleotide sequence of interest flanked by non-identical **recombination** sites and introducing into the plant cell a chimeric RNA-DNA oligonucleotide molecule. The chimeric RNA-DNA oligonucleotide is capable of recognizing and implementing a nucleotide conversion in one of the non-identical **recombination** sites so as to create two identical **recombination** sites. An appropriate recombinase is provided which excises the sequences between the two identical **recombination** sites.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:254223 USPATFULL
TITLE: Compositions and methods for the targeted removal of a nucleotide sequence from the genome of a plant
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States
Bowen, Benjamin A., Berkeley, CA, United States
Peterson, David J., Ames, IA, United States
Tagliani, Laura A., Zionsville, IN, United States
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6458594	B1	20021001
APPLICATION INFO.:	US 1999-439158		19991112 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2001

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)
	US 1998-98235P	19980828 (60)
	US 1997-65628P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Fox, David T.
ASSISTANT EXAMINER: Kruse, David H
LEGAL REPRESENTATIVE: Alston & Bird LLP
NUMBER OF CLAIMS: 30
EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 1619
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 20 OF 27 USPATFULL on STN
TI Compositions and methods to stack multiple nucleotide sequences of interest in the genome of a plant
AB Methods and compositions for the stacking of multiple nucleotide sequences at precise locations in the genome of a plant or plant cell are provided, Specifically, transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase. The transfer cassettes and target sites are designed so as to allow for the stacking or ordering of nucleotide sequences at precise locations in the plant genome.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:246589 USPATFULL
TITLE: Compositions and methods to stack multiple nucleotide sequences of interest in the genome of a plant
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States
Bowen, Benjamin A., Des Moines, IA, United States
Peterson, David J., Ames, IA, United States
Tagliani, Laura A., Ankeny, IA, United States
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6455315	B1	20020924
APPLICATION INFO.:	US 1999-438874		19991112 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2000

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-65627P	19971118 (60)
	US 1997-65613P	19971118 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Fox, David T.
ASSISTANT EXAMINER: Kruse, David H
LEGAL REPRESENTATIVE: Alston & Bird LLP
NUMBER OF CLAIMS: 44
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 1695
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 21 OF 27 USPATFULL on STN
TI Modified ribulose 1,5-bisphosphate carboxylase/oxygenase for improvement and optimization of plant phenotypes
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having Rubisco biosynthetic enzyme activities which are useful for,introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2001:183179 USPATFULL
TITLE: Modified ribulose 1,5-bisphosphate carboxylase/oxygenase for improvement and optimization of plant phenotypes
INVENTOR(S): Stemmer, Willem P.C., Los Gatos, CA, United States
Subramanian, Venkitswaran, San Diego, CA, United States
Zhu, Genhai, Sunnyvale, CA, United States
Liu, Lu, Redwood City, CA, United States
Selifonov, Sergey A., Los Altos, CA, United States
PATENT ASSIGNEE(S): Maxygen. Inc. (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2001032342	A1	20011018
APPLICATION INFO.:	US 2001-800123	A1	20010305 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1999-437726, filed on 9 Nov 1999, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1999-153093P	19990909 (60)
	US 1998-107756P	19981110 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
NUMBER OF CLAIMS: 26
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 5 Drawing Page(s)
LINE COUNT: 3440
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 22 OF 27 USPATFULL on STN
TI Compositions and methods for genetic modification of plants
AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:22439 USPATFULL
TITLE: Compositions and methods for genetic modification of plants
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States
Bowen, Benjamin A., Des Moines, IA, United States
Peterson, David J., Ames, IA, United States
Tagliani, Laura A., Ankeny, IA, United States
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6187994	B1	20010213
APPLICATION INFO.:	US 1998-193502		19981117 (9)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1997-65627, filed on 18 Nov 1997 Continuation of Ser. No. US 1997-65613, filed on 18 Nov 1997

	NUMBER	DATE

PRIORITY INFORMATION:	US 1997-45121P	19970430 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	Granted	
PRIMARY EXAMINER:	McElwain, Elizabeth F.	
ASSISTANT EXAMINER:	Mehta, Ashwin D.	
LEGAL REPRESENTATIVE:	Alston & Bird LLP	
NUMBER OF CLAIMS:	28	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	2 Drawing Figure(s); 2 Drawing Page(s)	
LINE COUNT:	1628	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 23 OF 27 USPATFULL on STN

TI Mammalian artificial chromosomes and methods of using same

AB The present invention provides a mammalian artificial chromosome (MAC), comprising a centromere and a unique cloning site, said MAC containing less than 0.1% of the DNA present in a normal haploid genome of the mammalian cell from which the centromere was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of preparing a MAC. In addition, the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC containing the selectable marker into the cell. The invention also provides a cell containing a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2000:138587 USPATFULL	
TITLE:	Mammalian artificial chromosomes and methods of using same	
INVENTOR(S):	Scheffler, Immo E., Del Mar, CA, United States	
PATENT ASSIGNEE(S):	The Regents of the University of California, Oakland, CA, United States (U.S. corporation)	

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6133503		20001017
APPLICATION INFO.:	US 1998-24472		19980217 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1996-741406, filed on 29 Oct 1996, now patented, Pat. No. US 5721118		

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-39256P	19951031 (60)
DOCUMENT TYPE:	Utility	
FILE SEGMENT:	Granted	
PRIMARY EXAMINER:	Campell, Bruce R.	
ASSISTANT EXAMINER:	Woitach, Joseph	
LEGAL REPRESENTATIVE:	Campbell & Flores LLP	
NUMBER OF CLAIMS:	14	
EXEMPLARY CLAIM:	1	
NUMBER OF DRAWINGS:	6 Drawing Figure(s); 3 Drawing Page(s)	
LINE COUNT:	1897	

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 24 OF 27 USPATFULL on STN

TI Mice homozygous for an inactivated α 1,3-galactosyl transferase gene

AB Human pre-formed xenoantibodies play an important role in the hyperacute rejection response in human xenotransplantation. Disclosed are materials and methods for removing or neutralizing such antibodies. Also disclosed are materials and methods for reducing or eliminating the epitopes in

the donor organs that are recognized by such antibodies. Such epitopes are formed as the result of activity by the enzyme α-1,3 galactosyltransferase. The porcine gene encoding α-1,3 galactosyltransferase is disclosed, as are materials and methods for inactivating ("knocking out") the α-1,3 galactosyltransferase gene in mammalian cells and embryos. Included are nucleic acid constructs useful for inactivating the α-1,3 galactosyltransferase gene in a target cell. Also disclosed is a novel leukemia inhibitory factor (T-LIF) that is useful for maintenance of embryonic stem cells and primordial germ cells in culture.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1998:157587 USPATFULL
TITLE:	Mice homozygous for an inactivated α 1,3-galactosyl transferase gene
INVENTOR(S):	d'Apice, Anthony J. F., Balwyn, Australia Pearse, Martin J., Mordialloc, Australia Robins, Allan J., Waterloo Corner, Australia Crawford, Robert J., West Lake Shores, Australia Rathjen, Peter D., Blackwood, Australia
PATENT ASSIGNEE(S):	Bresatch Limited, Adelaide, Australia (non-U.S. corporation) St. Vincent's Hospital, Victoria, Australia (non-U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5849991		19981215
APPLICATION INFO.:	US 1995-378617		19950126 (8)
RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1994-188607, filed on 27 Jan 1994, now abandoned		
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	Granted		
PRIMARY EXAMINER:	Crouch, Deborah		
LEGAL REPRESENTATIVE:	Fish & Richardson P.C., P.A.		
NUMBER OF CLAIMS:	13		
EXEMPLARY CLAIM:	5		
NUMBER OF DRAWINGS:	47 Drawing Figure(s); 42 Drawing Page(s)		
LINE COUNT:	4190		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 25 OF 27 USPATFULL on STN

TI Mammalian artificial chromosomes and methods of using same

AB The present invention provides a mammalian artificial chromosome (MAC), comprising a centromere and a unique cloning site, said MAC containing less than 0.1% of the DNA present in a normal haploid genome of the mammalian cell from which the centromere was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of preparing a MAC. In addition, the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC containing the selectable marker into the cell. The invention also provides a cell containing a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1998:19593 USPATFULL
TITLE:	Mammalian artificial chromosomes and methods of using same
INVENTOR(S):	Scheffler, Immo E., Del Mar, CA, United States
PATENT ASSIGNEE(S):	The Regents of the University of California, San Diego, Alameda, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5721118		19980224
APPLICATION INFO.:	US 1996-741406		19961029 (8)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1995-39256P	19951031 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Chambers, Jasemine C.
ASSISTANT EXAMINER: Schmuck, Jill D.
LEGAL REPRESENTATIVE: Campbell & Flores LLP
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 2,7,17
NUMBER OF DRAWINGS: 6 Drawing Figure(s); 3 Drawing Page(s)
LINE COUNT: 1797
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 26 OF 27 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

TI High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2μm plasmid system.

AB The best candidate for a high-copy-number and mitotic **stability** expression system in yeast is the endogenous 2μm plasmid. Nevertheless, derivatives of the 2μm plasmid typically exhibit lower copy numbers and require selection for adequate maintenance within cells. We report the construction and utilization of an efficient heterologous gene expression system containing a 4.5-kb inducible expression cassette inserted into the 2μm plasmid and selected in cells utilizing a carrier plasmid which is subsequently lost via **FRT/Flp recombination**.
The non-selectable 2μm plasmid, containing the cassette, was found to be stably maintained in cells, without selection, at high copy number. The dynamics of resolution and partitioning of this plasmid were analyzed during the course of 50 generations of growth under non-selective conditions. The heterologous lacZ reporter gene coding for β-galactosidase (βGal) is driven by the hybrid, galactose-inducible promoter GAL10::pMFα1. Upon induction, βGal was secreted into the periplasm and culture supernatant at levels which could be detected directly from Coomassie blue-stained SDS-PAGE. Furthermore, plasmid-containing cells could be maintained directly on rich YPD medium and identified either by utilizing XGal or by observing inhibition of colony growth on YPGal solid medium. The cassette was designed for direct, high-level, inducible expression of cloned genes downstream from the MFα1 signal sequence, with or without a C-terminal lacZ fusion. This vector represents the first demonstration of a non-selectable, mitotically stable, episomal plasmid system capable of expressing recombinant proteins at high levels. By supplanting the need for synthetic medium, this system could provide both an efficient and cost-effective means of generating recombinant protein at either the laboratory or large-scale level.

ACCESSION NUMBER: 93310911 EMBASE
DOCUMENT NUMBER: 1993310911
TITLE: High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2μm plasmid system.
AUTHOR: Ludwig D.L.; Ugolini S.; Bruschi C.V.
CORPORATE SOURCE: Microbiology Department, Internat. Ct. Gen. Eng./Biotechnol., Padriciano 99,I-34012 Trieste, Italy
SOURCE: Gene, (1993) 132/1 (33-40).
ISSN: 0378-1119 CODEN: GENED6
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English

SUMMARY LANGUAGE: English

L7 ANSWER 27 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2-mu-m plasmid system.
AB The best candidate for a high-copy-number and mitotic **stability** expression system in yeast is the endogenous 2-mu-m plasmid. Nevertheless, derivatives of the 2-mu-m plasmid typically exhibit lower copy numbers and require selection for adequate maintenance within cells. We report the construction and utilization of an efficient heterologous gene expression system containing a 4.5-kb inducible expression cassette inserted into the 2-mu-m plasmid and selected in cells utilizing a carrier plasmid which is subsequently lost via **FRT/Flp recombination**. The non-selectable 2-mu-m plasmid, containing the cassette, was found to be stably maintained in cells, without selection, at high copy number. The dynamics of resolution and partitioning of this plasmid were analyzed during the course of 50 generations of growth under non-selective conditions. The heterologous lacZ reporter gene coding for beta-galactosidase (beta-Gal) is driven by the hybrid, galactose-inducible promoter GAL10::pMF-alpha-1. Upon induction, beta-Gal was secreted into the periplasm and culture supernatant at levels which could be detected directly from Coomassie blue-stained SDS-PAGE. Furthermore, plasmid-containing cells could be maintained directly on rich YPD medium and identified either by utilizing XGal or by observing inhibition of colony growth on YPGal solid medium. The cassette was designed for direct, high-level, inducible expression of cloned genes downstream from the MF-alpha-1 signal sequence, with or without a C-terminal lacZ fusion. This vector represents the first demonstration of a non-selectable, mitotically stable, episomal plasmid system capable of expressing recombinant proteins at high levels. By supplanting the need for synthetic medium, this system could provide both an efficient and cost-effective means of generating recombinant protein at either the laboratory or large-scale level.
ACCESSION NUMBER: 1993:585676 BIOSIS
DOCUMENT NUMBER: PREV199497005046
TITLE: High-level heterologous gene expression in Saccharomyces cerevisiae from a stable 2-mu-m plasmid system.
AUTHOR(S): Ludwig, Dale L.; Ugolini, Simone; Bruschi, Carlo V. [Reprint author]
CORPORATE SOURCE: Microbiol. Dep., Int. Centre Genetic Eng. and Biotechnol., Padriciano 99, I-34012 Trieste, Italy
SOURCE: Gene (Amsterdam), (1993) Vol. 132, No. 1, pp. 33-40. CODEN: GENED6. ISSN: 0378-1119.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Dec 1993
Last Updated on STN: 28 Dec 1993

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=> d his

(FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'
ENTERED AT 17:55:41 ON 29 MAR 2004
L1 0 S FRT/FLP
L2 6180 S FRT OR FLP
L3 1238 S CRE LOX
L4 0 S L2 AND STABLE RECOMBINATION
L5 96 S FRT () FLP
L6 82 S L5 AND RECOMBINATION

```
L7            27 S L6 AND STABILITY
L8        583163 S HIS

=> s l7 and ARS
L9             0 L7 AND ARS

=> s autonomous replicating sequence
   4 FILES SEARCHED...
L10          217 AUTONOMOUS REPLICATING SEQUENCE

=> s l10 and l7
L11            0 L10 AND L7

=> s "1400 LNH-ST"
L12            0 "1400 LNH-ST"

=> s plasmid and "1400"
L13         5601 PLASMID AND "1400"

=> s XR or XD or XK
L14        16569 XR OR XD OR XK

=> s l14 and l7
L15            0 L14 AND L7

=> d his

     (FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

     FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'
     ENTERED AT 17:55:41 ON 29 MAR 2004
L1             0 S FRT/FLP
L2          6180 S FRT OR FLP
L3          1238 S CRE LOX
L4             0 S L2 AND STABLE RECOMBINATION
L5            96 S FRT () FLP
L6            82 S L5 AND RECOMBINATION
L7            27 S L6 AND STABILITY
L8        583163 S HIS
L9             0 S L7 AND ARS
L10          217 S AUTONOMOUS REPLICATING SEQUENCE
L11            0 S L10 AND L7
L12            0 S "1400 LNH-ST"
L13         5601 S PLASMID AND "1400"
L14        16569 S XR OR XD OR XK
L15            0 S L14 AND L7

=> s l3 and l10
L16            7 L3 AND L10

=> d l16 ti abs ibib tot

L16  ANSWER 1 OF 7  USPATFULL on STN
TI     Methods for isolating centromere DNA
AB     The invention provides efficient methods for the isolation of
       centromeres from potentially any organism. The methods represents an
       advance over the prior art in that costly and labor intensive mapping
       programs are not required. Using the technique, methylated centromere
       DNA may be isolated from potentially any centromere in an organism. The
       technique is amenable to mass screenings employing use of arrays
       comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER:       2004:31144  USPATFULL
```

TITLE: Methods for isolating centromere DNA
INVENTOR(S): Luo, Song, Chicago, IL, UNITED STATES
Copenhaver, Gregory, Oak Park, IL, UNITED STATES
Keith, Kevin, Chicago, IL, UNITED STATES
Preuss, Daphne, Chicago, IL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2004023282	A1	20040205
APPLICATION INFO.:	US 2003-620924	A1	20030716 (10)

RELATED APPLN. INFO.: Division of Ser. No. US 2001-888220, filed on 22 Jun 2001, GRANTED, Pat. No. US 6649347

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-228793P	20000623 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BELL, BOYD & LLOYD LLC, P.O. Box 1135, Chicago, IL, 60690-1135
NUMBER OF CLAIMS: 119
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 40 Drawing Page(s)
LINE COUNT: 4102
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 2 OF 7 USPATFULL on STN
TI Methods for generating or increasing revenues from crops
AB The present invention provides methods of doing business and providing services. For example, methods of increasing the revenue of crops are provided. To this end, the method includes the use of a nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and mini chromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:189578 USPATFULL
TITLE: Methods for generating or increasing revenues from crops
INVENTOR(S): Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES
Keith, Kevin, Chicago, IL, UNITED STATES
Preuss, Daphne, Chicago, IL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003131372	A1	20030710
APPLICATION INFO.:	US 2002-170944	A1	20020612 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-48451P	19970603 (60)
	US 1998-73741P	19980205 (60)
	US 1999-125219P	19990318 (60)
	US 1999-127409P	19990401 (60)
	US 1999-134770P	19990518 (60)
	US 1999-153584P	19990913 (60)
	US 1999-154603P	19990917 (60)
	US 1999-172493P	19991216 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Bell, Boyd & Lloyd LLC, P.O. Box 1135, Chicago, IL, 60690-1135
NUMBER OF CLAIMS: 91
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 46 Drawing Page(s)
LINE COUNT: 4575
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 3 OF 7 USPATFULL on STN
TI Plant centromere compositions
AB The present invention provides for the nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:180731 USPATFULL
TITLE: Plant centromere compositions
INVENTOR(S): Mach, Jennifer, Chicago, IL, UNITED STATES
Zieler, Helge, Chicago, IL, UNITED STATES
Jin, RongGuan, Chicago, IL, UNITED STATES
Keith, Kevin, Chicago, IL, UNITED STATES
Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES
Preuss, Daphne, Chicago, IL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003124561	A1	20030703
APPLICATION INFO.:	US 2002-170912	A1	20020612 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-48451P	19970603 (60)
	US 1998-73741P	19980205 (60)
	US 1999-125219P	19990318 (60)
	US 1999-127409P	19990401 (60)
	US 1999-134770P	19990518 (60)
	US 1999-153584P	19990913 (60)
	US 1999-154603P	19990917 (60)
	US 1999-172493P	19991216 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135
NUMBER OF CLAIMS: 127
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 46 Drawing Page(s)
LINE COUNT: 4478
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 4 OF 7 USPATFULL on STN
TI Methods for isolating centromere DNA
AB The invention provides efficient methods for the isolation of centromeres from potentially any organism. The methods represents an advance over the prior art in that costly and labor intensive mapping programs are not required. Using the technique, methylated centromere DNA may be isolated from potentially any centromere in an organism. The

technique is amenable to mass screenings employing use of arrays comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:227900 USPATFULL		
TITLE:	Methods for isolating centromere DNA		
INVENTOR(S):	Luo, Song, Chicago, IL, UNITED STATES Copenhaver, Gregory, Oak Park, IL, UNITED STATES Keith, Kevin, Chicago, IL, UNITED STATES Preuss, Daphne, Chicago, IL, UNITED STATES		
PATENT ASSIGNEE(S):	University of Chicago (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002123053	A1	20020905
	US 6649347	B2	20031118
APPLICATION INFO.:	US 2001-888220	A1	20010622 (9)
	NUMBER		DATE
PRIORITY INFORMATION:	US 2000-228793P		20000623 (60)
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135		
NUMBER OF CLAIMS:	119		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	40 Drawing Page(s)		
LINE COUNT:	4078		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 5 OF 7 USPATFULL on STN

TI Telomerase compositions and methods

AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of S. cerevisiae telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:108815 USPATFULL		
TITLE:	Telomerase compositions and methods		
INVENTOR(S):	Gottschling, Daniel E., Chicago, IL, United States Singer, Miriam S., Chicago, IL, United States		
PATENT ASSIGNEE(S):	Arch Development, Chicago, IL, United States (U.S. corporation)		
	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6387619	B1	20020514
APPLICATION INFO.:	US 1999-345294		19990630 (9)
RELATED APPLN. INFO.:	Division of Ser. No. US 1997-938534, filed on 26 Sep 1997, now patented, Pat. No. US 5916752 Division of Ser. No. US 1995-431080, filed on 28 Apr 1995, now patented, Pat. No. US 5698686 Division of Ser. No. US 345294 Continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned		
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	GRANTED		
PRIMARY EXAMINER:	Fredman, Jeffrey		
LEGAL REPRESENTATIVE:	Fulbright & Jaworski, LLP		
NUMBER OF CLAIMS:	10		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	15 Drawing Figure(s); 11 Drawing Page(s)		
LINE COUNT:	6648		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 6 OF 7 USPATFULL on STN
TI Telomerase screening methods
AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of S. cerevisiae telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1999:72446 USPATFULL
TITLE:	Telomerase screening methods
INVENTOR(S):	Gottschling, Daniel E., Chicago, IL, United States Singer, Miriam S., Chicago, IL, United States
PATENT ASSIGNEE(S):	Arch Development Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5916752		19990629
APPLICATION INFO.:	US 1997-938534		19970926 (8)

RELATED APPLN. INFO.:	Division of Ser. No. US 1995-431080, filed on 28 Apr 1995, now patented, Pat. No. US 5698686 which is a continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned
DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	Fredman, Jeffrey
LEGAL REPRESENTATIVE:	Arnold, White & Durkee
NUMBER OF CLAIMS:	56
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	15 Drawing Figure(s); 15 Drawing Page(s)
LINE COUNT:	7780

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 7 OF 7 USPATFULL on STN
TI Yeast telomerase compositions
AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of S. cerevisiae telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	97:118172 USPATFULL
TITLE:	Yeast telomerase compositions
INVENTOR(S):	Gottschling, Daniel E., Chicago, IL, United States Singer, Miriam S., Chicago, IL, United States
PATENT ASSIGNEE(S):	Arch Development Corporation, Chicago, IL, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 5698686		19971216
APPLICATION INFO.:	US 1995-431080		19950428 (8)

RELATED APPLN. INFO.:	Continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned
DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	Jones, W. Gary
ASSISTANT EXAMINER:	Fredman, Jeffrey
LEGAL REPRESENTATIVE:	Arnold, White & Durkee
NUMBER OF CLAIMS:	71
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	15 Drawing Figure(s); 15 Drawing Page(s)
LINE COUNT:	7319

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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=> d his

     (FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

     FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'
     ENTERED AT 17:55:41 ON 29 MAR 2004
L1             0 S FRT/FLP
L2          6180 S FRT OR FLP
L3          1238 S CRE LOX
L4             0 S L2 AND STABLE RECOMBINATION
L5            96 S FRT () FLP
L6            82 S L5 AND RECOMBINATION
L7            27 S L6 AND STABILITY
L8        583163 S HIS
L9             0 S L7 AND ARS
L10          217 S AUTONOMOUS REPLICATING SEQUENCE
L11            0 S L10 AND L7
L12            0 S "1400 LNH-ST"
L13         5601 S PLASMID AND "1400"
L14        16569 S XR OR XD OR XK
L15            0 S L14 AND L7
L16            7 S L3 AND L10

=> s l2 and l10
L17            8 L2 AND L10

=> d l17 ti abs ibib tot

L17  ANSWER 1 OF 8  USPATFULL on STN
TI     Methods for isolating centromere DNA
AB     The invention provides efficient methods for the isolation of
       centromeres from potentially any organism. The methods represents an
       advance over the prior art in that costly and labor intensive mapping
       programs are not required. Using the technique, methylated centromere
       DNA may be isolated from potentially any centromere in an organism. The
       technique is amenable to mass screenings employing use of arrays
       comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER:        2004:31144  USPATFULL
TITLE:                   Methods for isolating centromere DNA
INVENTOR(S):             Luo, Song, Chicago, IL, UNITED STATES
                         Copenhaver, Gregory, Oak Park, IL, UNITED STATES
                         Keith, Kevin, Chicago, IL, UNITED STATES
                         Preuss, Daphne, Chicago, IL, UNITED STATES

                              NUMBER        KIND    DATE
                         --------------- ------ --------
PATENT INFORMATION:      US 2004023282      A1   20040205
APPLICATION INFO.:       US 2003-620924     A1   20030716  (10)
RELATED APPLN. INFO.:    Division of Ser. No. US 2001-888220, filed on 22 Jun
                         2001, GRANTED, Pat. No. US 6649347

                                NUMBER         DATE
                         ------------------ --------
PRIORITY INFORMATION:    US 2000-228793P    20000623 (60)
DOCUMENT TYPE:           Utility
FILE SEGMENT:            APPLICATION
LEGAL REPRESENTATIVE:    BELL, BOYD & LLOYD LLC, P.O. Box 1135, Chicago, IL,
                         60690-1135
NUMBER OF CLAIMS:        119
EXEMPLARY CLAIM:         1
NUMBER OF DRAWINGS:      40 Drawing Page(s)
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LINE COUNT: 4102
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 2 OF 8 USPATFULL on STN
TI Methods for generating or increasing revenues from crops
AB The present invention provides methods of doing business and providing services. For example, methods of increasing the revenue of crops are provided. To this end, the method includes the use of a nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and mini chromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:189578 USPATFULL
TITLE: Methods for generating or increasing revenues from crops
INVENTOR(S): Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES
Keith, Kevin, Chicago, IL, UNITED STATES
Preuss, Daphne, Chicago, IL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003131372	A1	20030710
APPLICATION INFO.:	US 2002-170944	A1	20020612 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-48451P	19970603 (60)
	US 1998-73741P	19980205 (60)
	US 1999-125219P	19990318 (60)
	US 1999-127409P	19990401 (60)
	US 1999-134770P	19990518 (60)
	US 1999-153584P	19990913 (60)
	US 1999-154603P	19990917 (60)
	US 1999-172493P	19991216 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Bell, Boyd & Lloyd LLC, P.O. Box 1135, Chicago, IL, 60690-1135
NUMBER OF CLAIMS: 91
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 46 Drawing Page(s)
LINE COUNT: 4575
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 3 OF 8 USPATFULL on STN
TI Plant centromere compositions
AB The present invention provides for the nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:180731 USPATFULL
TITLE: Plant centromere compositions
INVENTOR(S): Mach, Jennifer, Chicago, IL, UNITED STATES
Zieler, Helge, Chicago, IL, UNITED STATES
Jin, RongGuan, Chicago, IL, UNITED STATES

Keith, Kevin, Chicago, IL, UNITED STATES
Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES
Preuss, Daphne, Chicago, IL, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003124561	A1	20030703
APPLICATION INFO.:	US 2002-170912	A1	20020612 (10)

RELATED APPLN. INFO.: Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING

	NUMBER	DATE
PRIORITY INFORMATION:	US 1997-48451P	19970603 (60)
	US 1998-73741P	19980205 (60)
	US 1999-125219P	19990318 (60)
	US 1999-127409P	19990401 (60)
	US 1999-134770P	19990518 (60)
	US 1999-153584P	19990913 (60)
	US 1999-154603P	19990917 (60)
	US 1999-172493P	19991216 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135
NUMBER OF CLAIMS: 127
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 46 Drawing Page(s)
LINE COUNT: 4478
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 4 OF 8 USPATFULL on STN
TI Rapid creation of gene targeting vectors using homologous recombination in yeast
AB The present invention provides methods of preparing gene targeted mammalian cells having a targeted gene mutation methods of making gene targeted mice, and gene targeting vectors that are useful in these methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:134098 USPATFULL
TITLE: Rapid creation of gene targeting vectors using homologous recombination in yeast
INVENTOR(S): Fisher, Katherine E., Old Lyme, CT, UNITED STATES
Reaume, Andrew G., Waterford, CT, UNITED STATES

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2003092183	A1	20030515
APPLICATION INFO.:	US 2001-961163	A1	20010921 (9)

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Gregg C. Benson, Pfizer Inc., Patent Department, MS 4159, Eastern Point Road, Groton, CT, 06340
NUMBER OF CLAIMS: 20
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Page(s)
LINE COUNT: 1249
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 5 OF 8 USPATFULL on STN

TI Methods for isolating centromere DNA

AB The invention provides efficient methods for the isolation of centromeres from potentially any organism. The methods represents an advance over the prior art in that costly and labor intensive mapping programs are not required. Using the technique, methylated centromere DNA may be isolated from potentially any centromere in an organism. The technique is amenable to mass screenings employing use of arrays comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:227900 USPATFULL			
TITLE:	Methods for isolating centromere DNA			
INVENTOR(S):	Luo, Song, Chicago, IL, UNITED STATES Copenhaver, Gregory, Oak Park, IL, UNITED STATES Keith, Kevin, Chicago, IL, UNITED STATES Preuss, Daphne, Chicago, IL, UNITED STATES			
PATENT ASSIGNEE(S):	University of Chicago (U.S. corporation)			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002123053	A1	20020905	
	US 6649347	B2	20031118	
APPLICATION INFO.:	US 2001-888220	A1	20010622	(9)
	NUMBER		DATE	
PRIORITY INFORMATION:	US 2000-228793P		20000623	(60)
DOCUMENT TYPE:	Utility			
FILE SEGMENT:	APPLICATION			
LEGAL REPRESENTATIVE:	BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135			
NUMBER OF CLAIMS:	119			
EXEMPLARY CLAIM:	1			
NUMBER OF DRAWINGS:	40 Drawing Page(s)			
LINE COUNT:	4078			

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 6 OF 8 USPATFULL on STN

TI Methods for the production of gelatin and full-length triple helical collagen in recombinant cells

AB Methods are disclosed for simplified recombinant production of fibrillar collagens. DNAs encoding fibrillar collagen monomers lacking the N propeptide, the C propeptide, or both propeptides are introduced into recombinant host cells and expressed. Trimeric collagen is recovered from the recombinant host cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	2002:194714 USPATFULL			
TITLE:	Methods for the production of gelatin and full-length triple helical collagen in recombinant cells			
INVENTOR(S):	Olsen, David R., Menlo Park, CA, United States Chang, Robert, Hillsborough, CA, United States McMullin, Hugh, Menlo Park, CA, United States Hitzeman, Ronald A., Pacifica, CA, United States Chisholm, George, San Mateo, CA, United States			
PATENT ASSIGNEE(S):	Cohesion Technologies, Inc., Palo Alto, CA, United States (U.S. corporation) Genotypes, Inc., Pacifica, CA, United States (U.S. corporation)			
	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6428978	B1	20020806	
APPLICATION INFO.:	US 1999-289578		19990409	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 1998-84828P	19980508 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Whisenant, Ethan C.
LEGAL REPRESENTATIVE: Osman, Richard Aron
NUMBER OF CLAIMS: 31
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 14 Drawing Figure(s); 14 Drawing Page(s)
LINE COUNT: 1945
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 7 OF 8 USPATFULL on STN
TI Recombinant gelatin and full-length triple helical collagen
AB Methods are disclosed for simplified recombinant production of fibrillar collagens. DNAs encoding fibrillar collagen monomers lacking the N propeptide, the C propeptide, or both propeptides are introduced into recombinant host cells and expressed. Trimeric collagen is recovered from the recombinant host cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:160549 USPATFULL
TITLE: Recombinant gelatin and full-length triple helical collagen
INVENTOR(S): Olsen, David R., Menlo Park, CA, United States
Chang, Robert, Hillsborough, CA, United States
McMullin, Hugh, Menlo Park, CA, United States
Hitzeman, Ronald A., Pacifica, CA, United States
Chisholm, George, San Mateo, CA, United States
PATENT ASSIGNEE(S): Cohesion Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)
Genotypes, Inc., Pacifica, CA, United States (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 6413742	B1	20020702
APPLICATION INFO.:	US 2000-585887		20000531 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1999-289578, filed on 9 Apr 1999

	NUMBER	DATE
PRIORITY INFORMATION:	US 1998-84828P	19980508 (60)

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Whisenant, Ethan C.
LEGAL REPRESENTATIVE: Osman, Richard Aron
NUMBER OF CLAIMS: 29
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 14 Drawing Figure(s); 14 Drawing Page(s)
LINE COUNT: 1573
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 8 OF 8 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
TI Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
AN 2000-587529 [55] WPIDS
CR 1999-080832 [07]; 2000-587463 [55]; 2003-829605 [77]
AB WO 200055325 A UPAB: 20031128
NOVELTY - A recombinant DNA construct (I) comprising a plant centromere,

is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a minichromosome vector comprising a plant centromere and telomere sequence;

(2) a cell transformed with a recombinant DNA construct comprising a plant centromere;

(3) a plant comprising the cell of (2);

(4) a method of preparing a transgenic plant cell comprising contacting a starting plant cell with a recombinant DNA construct comprising a plant centromere;

(5) a transgenic plant comprising a minichromosome vector;

(6) a method for producing a minichromosome vector comprising:

(a) obtaining a first and second vector, where either comprises a selectable or screenable marker, an origin of replication, a telomere, and a plant centromere, and where the vectors comprise a site for site-specific recombination; and

(b) contacting the first vector with the second vector;

(7) a method of screening a candidate centromere sequence for plant centromere activity comprising:

(a) obtaining an isolated nucleic acid sequence comprising a candidate centromere sequence;

(b) integratively transforming plant cells with the isolated nucleic acid; and

(c) screening for centromere activity;

(8) a recombinant DNA construct comprising an Arabidopsis polyubiquitin 11 promoter comprising a defined 2000 bp sequence (given in the specification), or its fragments;

(9) a recombinant DNA construct comprising an Arabidopsis 40S ribosomal protein S16 promoter comprising a defined 2000 bp sequence (given in the specification);

(10) a recombinant DNA construct comprising an Arabidopsis polyubiquitin 11 3' regulatory sequence comprising a defined 2001 bp sequence (given in the specification); and

(11) a recombinant DNA construct comprising an Arabidopsis 40S ribosomal protein S16 3' regulatory sequence comprising a defined 2000 bp sequence (given in the specification).

USE - The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.

Dwg.0/23

ACCESSION NUMBER: 2000-587529 [55] WPIDS

CROSS REFERENCE: 1999-080832 [07]; 2000-587463 [55]; 2003-829605 [77]

DOC. NO. CPI: C2000-175305

TITLE: Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.

DERWENT CLASS: B04 C06 D16 P13

INVENTOR(S): COPENHAVER, G; KEITH, K; PREUSS, D; JIN, R; MACH, J; ZIELER, H

PATENT ASSIGNEE(S): (UYCH-N) UNIV CHICAGO; (COPE-I) COPENHAVER G; (JINR-I) JIN R; (KEIT-I) KEITH K; (MACH-I) MACH J; (PREU-I) PREUSS D; (ZIEL-I) ZIELER H

COUNTRY COUNT: 91

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000055325 A2		20000921	(200055)*	EN	

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES
FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2000037649 A 20001004 (200101)
BR 2000009119 A 20011226 (200206)
EP 1165792 A2 20020102 (200209) EN
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL
US 2003124561 A1 20030703 (200345)

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000055325	A2		WO 2000-US7392	20000317
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BR 2000009119	A		BR 2000-9119	20000317
			WO 2000-US7392	20000317
EP 1165792	A2		EP 2000-916559	20000317
			WO 2000-US7392	20000317
US 2003124561	A1	Provisional	US 1997-48451P	19970603
		Provisional	US 1998-73741P	19980205
		Cont of	US 1998-90051	19980603
		Provisional	US 1999-125219P	19990318
		Provisional	US 1999-127409P	19990401
		Provisional	US 1999-134770P	19990518
		Provisional	US 1999-153584P	19990913
		Provisional	US 1999-154603P	19990917
		Provisional	US 1999-172493P	19991216
		CIP of	US 2000-531120	20000317
		CIP of	US 2000-553231	20000419
			US 2002-170912	20020612

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000037649	A	Based on	WO 2000055325
BR 2000009119	A	Based on	WO 2000055325
EP 1165792	A2	Based on	WO 2000055325
US 2003124561	A1	Cont of	US 6156953

PRIORITY APPLN. INFO: US 1999-172493P 19991216; US 1999-125219P 19990318; US 1999-127409P 19990401; US 1999-134770P 19990518; US 1999-153584P 19990913; US 1999-154603P 19990917; US 1997-48451P 19970603; US 1998-73741P 19980205; US 1998-90051 19980603; US 2000-531120 20000317; US 2000-553231 20000419; US 2002-170912 20020612

Refine Search

Search Results -

Terms	Documents
L10 and L1	1

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Search: L11

Refine Search

Recall Text | Clear | Interrupt

Search History

DATE: Monday, March 29, 2004 Printable Copy Create Case

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L9	L8 and l1	1	L9
L8	ARS	87461	L8
L7	l1 and l4	1	L7
L6	L5 and l1	1	L6
L5	integrative plasmid	37878	L5
L4	replicative plasmid	38012	L4
L3	l2 and l1	1	L3
L2	replicative and integrative plasmid	37405	L2
L1	5789210.pn.	1	L1

END OF SEARCH HISTORY

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First Hit Fwd Refs

End of Result Set

Generate Collection Print

L6: Entry 1 of 1 File: USPT Aug 4, 1998

DOCUMENT-IDENTIFIER: US 5789210 A

** See image for Certificate of Correction **

TITLE: Recombinant yeasts for effective fermentation of glucose and xylose

Drawing Description Text (4):
FIG. 3 shows the genes cloned on and the restriction map of the plasmid pLSK15.

Drawing Description Text (5):
FIG. 4 shows the genes cloned on and the restriction map of the plasmid pUCKm10.

Drawing Description Text (6):
FIG. 5 shows the genes cloned on and the restriction map of the plasmid pLNH21.

Drawing Description Text (10):
FIG. 7 shows the genes cloned on and the restriction map of plasmid pLNH33.

Drawing Description Text (13):
FIG. 9 is a schematic diagram outlining the construction of pBluescript II KS(-) containing the cloned XR, XD, and XK genes: four such plasmids were constructed: pKS(-)-KK-A*R-KD-1; pKS(-)-KK-A*R-KD-2; pKS(-)-KK-AR-KD-3; and pKS(-)-KK-AR-KD-4, as further described in Example 4.

Drawing Description Text (16):
FIG. 12 is a schematic diagram outlining the construction of the plasmid pLNH21.

Detailed Description Text (5):
The particular XR gene used in the applicants' studies herein was cloned from P. stipitis by Polymerase Chain Reaction (PCR) (Chen and Ho, 1993). The oligonucleotides required for the amplification of XR from the chromosomal DNA by PCR were synthesized according to the published sequence of the P. stipitis XR gene (Takama et al., 1991). The amplified XR was first cloned and stored into plasmid pUC19. The cloned XR was then fused to different promotors including the promotors of yeast TRP5 gene (Zalkin and Yanofsky, 1982) and yeast alcohol dehydrogenase I gene (ADC1) (Ammerer, 1983; Bennetzen and Hall, 1982).

Detailed Description Text (10):
The fusion of XR, XD, and XK to intact promoters from ADC1, PYK, GPD, etc., was carried out by cloning both the fragment containing the specific promoter and the structural gene of XR, XD, or XK on one of the Bluescript KS plasmids (Stratagene, La Jolla, Calif.), followed by the removal of the extra unwanted nucleotides by site-specific mutagenesis (Kunkel et al., 1987). The invention thus also provides several pBluescript II KS(-) (hereinafter pKS(-)) derivatives containing the cloned XD (fused to the pyruvate dehydrogenase promoter), XR (fused to the ADC1 promoter), and XK (fused to the pyruvate kinase promoter). These recombinant plasmids are designated as pKS(-) KD-AR (or A*R) -KK. Four such plasmids were constructed as outlined in FIG. 9. These plasmids have similar but not identical structures. The XR, XD, and XK (or KD-AR (or A*R) -KK) cloned on these plasmids can be separated from the parent pKS(-) plasmid by a single XhoI restriction digestion.

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Detailed Description Text (11):
The XR, XD, and XK genes fused to the proper promoters were then cloned on pLSK15 (FIG. 3) or pUCKm10 (FIG. 4). pLSK15, a derivative of pLX10-14 (Stevis and Ho, 1985), is a low copy number plasmid with a copy number of approximately 10 in yeast (S. cerevisiae). It contains the yeast 2.mu. replicon which enables the plasmid to be replicated autonomously in S. cerevisiae and closely related species. pLSK15 also contains the geneticin (kanamycin) resistance gene (Km.sup.R) and ampicillin resistance gene (Ap.sup.R and also amp.sup.r) which serve as selection markers in S. cerevisiae and other yeasts. pLSK15 also contains the XK gene fused to the yeast TRP-5 promoter. Thus, XR and XD genes fused to proper 5' noncoding sequences containing suitable promoters were inserted into pLSK15 to demonstrate the effect of the resulting plasmids on yeast xylose fermentation. To compare the effect of the presence of different genes on yeast xylose fermentation, a plasmid containing only XR and XD was also used to transform S. cerevisiae and the resulting yeast used in comparative fermentations. Results of the fermentation of xylose by un-engineered S. cerevisiae, yeast containing the cloned XR, XD, and XK (SC(pLNH21)), and yeast containing the cloned XR and XD but not XK (SC(pLNH13-32)) genes are shown in FIG. 6A, 6B, and 6C.

Detailed Description Text (12):
pUCKm10 (FIG. 4) is a high copy-number plasmid (i.e. plasmid with a copy number of about 50 or more) with a copy number close to 100 in S. cerevisiae. pUCKm10 is a pUC9 derivative containing the identical 2.mu. replicon, and the Km.sup.R, and Ap.sup.R genes present in pLSK15. These specific DNA fragments serve as the replicon and selection markers that enable the plasmid to be replicated autonomously in S. cerevisiae (and in related yeasts) and also enable the yeast transformants containing the plasmid to be distinguished from the untransformed host cells.

Detailed Description Text (13):
The applicants have constructed pUCKm10 based recombinant plasmids that contain the same XR, XD, and XK fused to 5' proper noncoding sequences containing suitable promotors. These vectors are designed to be useful to transform all S. cerevisiae strains and strains of related species. No special mutants are required to act as the recipient strains. Thus plasmids such as pLNH33 (FIG. 7), as well as pLNH21 (FIG. 5), can be used to transform industrial S. cerevisiae and other strains.

Detailed Description Text (14):
Yeast transformation with derivatives of either pLSK15 or pUCKm10 was carried out by electroporation generally using the the procedure described by Becker and Guarente (1991). Authentic yeast transformants containing derivatives of either pLSK15 or pUCKm10 were isolated as further described below. Km.sup.R present in the plasmids served as the primary selection marker which renders any host cells obtaining one of these plasmids resistant to a much higher concentration of geneticin present in the medium. However, some yeast cells can be induced to become resistant to the same level of geneticin of the transformants containing the plasmid. Thus, not every geneticin resistant colony is a true transformant. It has been reported that Ap.sup.R can be expressed in S. cerevisiae but the latter is resistant to ampicillin without the presence of Ap.sup.R. Thus, Ap.sup.R cannot serve as a selection marker for yeast plasmid-mediated transformation. Nevertheless, yeasts that contain the highly expressed Ap.sup.R will produce sufficient penicillinase and make it possible to identify colonies containing such yeasts on special solid plates by the penicillinase test (Chevallier and Aigle, 1979). The latter test has provided a technique to identify the true transformants of S. cerevisiae and other yeasts from the geneticin resistant colonies.

Detailed Description Text (18):
pLNH33 is a more effective plasmid than pLNH21 for xylose fermentation because it is a higher copy-number plasmid. Furthermore, the XK in pLNH33 is fused to a more

efficient promoter than the XK in pLNH21. S. cerevisiae has also been transformed with pLNH33, designated SC(pLNH33). Although SC(pLNH33) is much more effective in fermenting xylose or mixtures of xylose and glucose than SC(pLNH21), 1400(pLNH33) was found to be more effective in fermenting mixtures of glucose and xylose than SC (pLNH33). Thus, individual strains also affect the efficiency of fermentation. Similar to S. cerevisiae, the unengineered strain 1400 cannot use or ferment xylose (alone or in a mixture of glucose and xylose) as shown in FIG. 8B.

Detailed Description Text (30):
Oligonucleotides I and II were used to synthesize the intact XD gene and oligonucleotides II and III were used to synthesize the promotorless XD as shown in FIG. 10. The intact XD and the promotorless XD were first cloned in pKS(-) plasmid. The intact XR was then subcloned on pUCKm10 (FIG. 4) and the resulting plasmid pUCKm10-XD, was used to transform S. cerevisiae by electroporation as described in Example 5. The yeast transformants were used to assay the xylitol dehydrogenase activity to demonstrate that the cloned gene is intact and can be expressed in S. cerevisiae.

Detailed Description Text (34):
The promoter fragment of yeast pyruvate kinase from -910 to +23 (Burke et al., 1983) was synthesized by PCR as described in Example 1 for the synthesis of the XD gene. Both the P.sub.PK fragment and the promotorless XD were subcloned on pKS(-) plasmid and the undesired nucleotides between the P.sub.PK and the intact XD structural gene were removed by site-specific mutagenesis according to the procedure of Kunkel (Kunkel, 1987). The resulting fused gene contains -910 to -1 promoter fragments from the pyruvate kinase gene and +1 to +1963 nucleotides from the Pichia XD gene. The resulting pKS(-) plasmid containing P.sub.PK -XD (or KD) is designated pKS(-)-KD or pKD2.

Detailed Description Text (40):
Plasmid pMA56 (Ammerer, 1983) contains the yeast alcohol dehydrogenase I promoter (P.sub.ADC1). The applicants have used this promoter to modify some of the genes in their work. For example, P.sub.ADC1 has been fused to XR, and the resulting gene has been designated P.sub.ADC1 -XR or AR. Nevertheless, this P.sub.ADC1 is not intact and does not contain the -1 to -14 nucleotides of the intact ADC1 promoter (Bennetzen and Hall, 1982). The -1 to -14 region of a gene is usually very significant for controlling protein synthesis. Any gene fused to such a promoter has to rely on its original genetic signal for controlling the synthesis of its protein product.

Detailed Description Text (43):
Construction of plasmid pLNH21 (also designated as pLSK15-KD-AR) and transformation of S. cerevisiae and 1400 with pLNH21

Detailed Description Text (44):
The construction of pLNH21 is outlined in FIG. 12. pLNH21 was used to transform S. cerevisiae and strain 1400 by electroporation under the following conditions. Fifty ml yeast cells, grown to early log phase (Klett Unit (KU) 130), were centrifuged to remove the medium, washed twice with cold water, once with cold 1M sorbitol, and resuspended in 200 .mu.l 1M sorbitol. Sixty .mu.l of the cells were transferred into a 4 ml presterilized plastic tube (with cap) and to which 0.1 .mu.g to 1 .mu.g plasmid DNA was added. Fifty .mu.l of the resulting cells and plasmid mixture were pipetted into a precooled gene pulser cuvette with a 0.2 cm electrode gap and the content in the cuvette was subjected to pulse by the gene pulser with a pulse controller (BioRad) at 2.0 KV, 25 .mu.F, 200 ohms.

Detailed Description Text (46):
Transformation of strain 1400 with pLNH21 or other plasmids was carried out using a similar procedure to that described above, except that the cells were grown to 140-190 KU rather than 130 KU and the YEPD plates for the initial selection of

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transformants after electroporation contained 40 .mu.g/ml geneticin G418 rather than 50. Transformation of strain 1400 by the above described procedures was not as effective as transformation of S. cerevisiae.

Detailed Description Text (49):
These three yeasts were cultured in rich medium YEPD aerobically under identical conditions (SC(pLNH13-32) was constructed by transforming S. cerevisiae with a plasmid, designated pLNH13-32, which contains only the XR and XD gene/promotor combinations). These yeast cells were then used to ferment 5% xylose in YEP (1% yeast extract, 2% peptone) medium anaerobically also under identical conditions. The consumption of xylose and the formation of ethanol and xylitol were followed during fermentation by taking samples at proper intervals and analyzing them by HPLC under the following conditions.

Detailed Description Text (61):
When the cell density reached mid-log phase (400 Klett units), 12.5 ml (40%) glucose and 6.25 ml (40%) xylose were added to each flask. After thorough mixing, 1 ml of the culture mixture was removed from the flask to serve as the zero sample. The flask was then sealed with Saran wrap to allow fermentation to be carried out anaerobically. One ml samples of the fermentation broth (with some cells) were removed at proper intervals (every 24 hr.) to serve as samples for measuring the sugar and ethanol contents of the broth during fermentation. The ethanol, glucose, xylose, and xylitol contents of the samples were analyzed by HPLC as described in Example 6. The results, shown in FIGS. 8A and 8B, demonstrate that the genetically engineered yeast 1400(pLNH33) can ferment 10% glucose and 5% xylose to ethanol simultaneously in two to four days without requiring high cell density. On the other hand, the parent strain 1400 can only convert glucose to ethanol but not xylose. The fermentation was carried out under normal conditions, without requiring special medium, special pH, and also without requiring growth of yeast to high cell density. Thus the genetically engineered 1400(pLNH33) containing the XR, XD, and XK, all fused to glycolytic promotors and cloned on a high copy-number plasmid pUCKm10, can ferment high concentrations of both glucose and xylose simultaneously to ethanol in two to four days with very little xylitol produced as a by-product.

Detailed Description Text (78):
Chevallier, M. R. and M. Aigle, "Qualitative detection of penicillinase produced by yeast strains carrying chimeric yeast-coli plasmids," FEBS Letters, 108(1) 179-184 (1979).

Other Reference Publication (6):
Chevallier, M. R. and M. Aigle, "Qualitative detection of penicillinase produced by yeast strains carrying chimeric yeast-coli plasmids," FEBS Letters, 108(1) 179-184 (1979).

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L2            2 S E3
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L3            1 S E3
L4           26 S XYLOSE REDUCTASE
L5            7 S XYLITOL DEHYDROGENASE
L6           33 S XYLULOKINASE

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L7         2967 S L1-L6
L8          464 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE
L9         3153 S ALDOSE REDUCTASE
L10          68 S XYLULOSE REDUCTASE
L11          50 S XYLULOSE KINASE
L12        3760 S L7-L11
L13         218 S L12 AND YEAST
                E YEAST/CT
L14          25 S L12 AND E3-E53
                E E53+ALL
L15       12225 S E1
                E E2+ALL
L16       34588 S E6,E5+NT
L17          25 S  L12 AND L15,L16
L18         218 S L13,L14,L17
L19           1 S YEAST(L)1400(L)LNH(L)ST
                E SACCHAROMYCES/CT
L20           9 S L12 AND E3
L21         114 S L12 AND E3-E196
                E E3+ALL
L22           0 S L12 AND E4
L23         113 S L12 AND E5+NT
L24         269 S L18,L20-L23
L25          32 S L24 AND DNA
L26          31 S L24 AND PLASMID
L27          20 S L24 AND CHROMOSOM?
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L29          74 S L24 AND GENETIC?/SC,SX
L30         130 S L25-L29
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L34          20 S E3,E11,E12
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                E CHEN Z/AU
L36         722 S E3,E7
                E CHEN ZHENG/AU
L37         261 S E3,E4
L38           8 S E51
L39           1 S L31 AND L32,L33
L40          11 S L31 AND L34-L38
L41          11 S L32,L33,L39,L40
L42         134 S L31 AND (PD<=19960506 OR PRD<=19960506 OR AD<=19960506)
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L48            2 S E1-E6 AND L47
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                 SEL HIT RN

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L50           14 S E7-E20
L51           14 S L50 AND L1-L6

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http://www.cas.org/ONLINE/DBSS/registryss.html

=> d ide can tot l51

L51  ANSWER 1 OF 14  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   183399-64-6  REGISTRY
CN   DNA (Pachysolen tannophilus clone pBS1554 aldose reductase gene plus
     flanks) (9CI)  (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN   Deoxyribonucleic acid (Pachysolen tannophilus clone pBS1554 aldose
     reductase gene plus 5'- and 3'-flanking region fragment)
OTHER NAMES:
CN   Deoxyribonucleic acid (Pachysolen tannophilus clone pBS1554 aldose
     (xylose) reductase gene plus 5'- and 3'-flanking region fragment)
CN   GenBank U40706
FS   NUCLEIC ACID SEQUENCE
MF   Unspecified
CI   MAN
SR   GenBank
LC   STN Files:   BIOSIS, CA, CAPLUS, GENBANK

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REFERENCE   1:  126:2045
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L51 ANSWER 2 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **183327-22-2** REGISTRY
CN Reductase, aldose (Pachysolen tannophilus clone pBS1554 reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **Aldose (xylose) reductase (Pachysolen tannophilus clone pBS1554 reduced) (E.C. 1.1.1.21)**
CN GenBank AAC49526
CN GenBank AAC49526 (Translated from: GenBank U40706)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS

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*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 126:2045

L51 ANSWER 3 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **167974-35-8** REGISTRY
CN **DNA (Saccharomyces cerevisiae strain 1400 clone pLNH33 xylulokinase gene plus flanks) (9CI)** (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN **Deoxyribonucleic acid (Saccharomyces cerevisiae strain 1400 clone pLNH33 xylulokinase gene plus 5'- and 3'-flanking region fragment)**
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 123:196764

L51 ANSWER 4 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **167078-89-9** REGISTRY
CN **Xylulokinase (Saccharomyces cerevisiae strain 1400 clone pLNH33 reduced) (9CI)** (CA INDEX NAME)
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

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1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 123:196764

L51 ANSWER 5 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **146409-22-5** REGISTRY
CN DNA (Yamadazyma stipitis clone pUA103 gene XYL1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **Deoxyribonucleic acid (Pichia stipitis xylose reductase gene XYL1)**
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS

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REFERENCE 1: 118:123016

L51 ANSWER 6 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **146409-21-4** REGISTRY
CN DNA (Yamadazyma stipitis clone pUA103 gene XYL1 plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **Deoxyribonucleic acid (Pichia stipitis xylose reductase gene XYL1 plus 5'- and 3'-flanking region fragment)**
FS NUCLEIC ACID SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
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1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 118:123016

L51 ANSWER 7 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **138263-97-5** REGISTRY
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **NADH/NADPH-dependent xylose reductase (Pichia stipitis reduced)**
CN **Xylose reductase (Pichia stipitis reduced)**
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

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REFERENCE 1: 118:226769

REFERENCE 2: 118:123016

REFERENCE 3: 118:96990

REFERENCE 4: 116:52957

REFERENCE 5: 116:35663

L51 ANSWER 8 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **121548-71-8** REGISTRY
CN Protein (Saccharomyces cerevisiae gene GCY reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 40: PN: WO0155342 SEQID: 42 claimed protein
CN Protein (Saccharomyces cerevisiae clone pEOA306/pEOA265/pEOA106 gene GCY)
CN Protein (Saccharomyces cerevisiae clone pEOA347 gene GCY)
CN Protein (Saccharomyces cerevisiae gene GCY1)
CN Reductase, aldose (Saccharomyces cerevisiae gene AKR-A)
CN **Xylose reductase (Saccharomyces cerevisiae open reading frame YJR096W)**
FS PROTEIN SEQUENCE
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL

RELATED SEQUENCES AVAILABLE WITH SEQLINK

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
*** USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE ***
6 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
6 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 136:2117

REFERENCE 2: 135:148225

REFERENCE 3: 127:219657

REFERENCE 4: 127:131709

REFERENCE 5: 124:252209

REFERENCE 6: 111:34409

L51 ANSWER 9 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **104118-53-8** REGISTRY
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **D-Xylose reductase**
CN **D-Xylose reductase (NADPH)**
CN **NADPH-dependent xylose reductase**
CN Reductase, xylose (reduced nicotinamide adenine dinucleotide phosphate)
CN **Xylose reductase**
DR 163913-54-0
MF Unspecified
CI MAN
SR CA
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, TOXCENTER

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
29 REFERENCES IN FILE CA (1907 TO DATE)

29 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:107416

REFERENCE 2: 140:14605

REFERENCE 3: 138:400479

REFERENCE 4: 138:86217

REFERENCE 5: 137:335006

REFERENCE 6: 135:223422

REFERENCE 7: 135:136473

REFERENCE 8: 133:360695

REFERENCE 9: 132:11668

REFERENCE 10: 131:227744

L51 ANSWER 10 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **99775-25-4** REGISTRY
CN Reductase, D-xylose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **D-Xylose reductase**
CN **NADH-dependent xylose reductase**
CN **Xylose reductase**
MF Unspecified
CI MAN
SR CA
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
51 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
51 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 139:225259

REFERENCE 2: 139:178733

REFERENCE 3: 139:65901

REFERENCE 4: 138:283215

REFERENCE 5: 138:166431

REFERENCE 6: 138:54597

REFERENCE 7: 138:54591

REFERENCE 8: 137:139426

REFERENCE 9: 137:30383

REFERENCE 10: 136:147534

L51 ANSWER 11 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **95829-40-6** REGISTRY
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide

(phosphate)) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **D-Xylose reductase**
CN NAD(P)H-dependent aldose reductase
CN **NAD(P)H-dependent xylose reductase**
CN **NADPH-D-xylose reductase**
CN **Xylose reductase**
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
79 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
79 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:107416

REFERENCE 2: 140:55544

REFERENCE 3: 140:14605

REFERENCE 4: 139:394971

REFERENCE 5: 139:394931

REFERENCE 6: 139:360858

REFERENCE 7: 139:260078

REFERENCE 8: 139:260077

REFERENCE 9: 139:226255

REFERENCE 10: 139:176481

L51 ANSWER 12 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **9030-58-4** REGISTRY
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN **D-Xylulokinase**
CN D-Xylulose kinase
CN E.C. 2.7.1.17
CN **Xylulokinase**
CN Xylulose kinase
DR 57127-28-3
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CIN, EMBASE, PIRA, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
154 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
154 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:144753

REFERENCE 2: 140:127260

REFERENCE 3: 140:107886

REFERENCE 4: 139:347843

REFERENCE 5: 139:260078

REFERENCE 6: 139:260077

REFERENCE 7: 139:226997

REFERENCE 8: 139:225259

REFERENCE 9: 139:178733

REFERENCE 10: 139:163668

L51 ANSWER 13 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **9028-31-3** REGISTRY
CN Reductase, aldose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Aldose reductase
CN D-Ribose reductase
CN E.C. 1.1.1.21
CN L-Arabinose reductase
CN NADPH-aldopentose reductase
CN NADPH-aldose reductase
CN NADPH-dependent aldose reductase
CN NADPH-L-arabinose reductase
CN **Xylose reductase**
MF Unspecified
CI MAN
LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CEN, CIN, EMBASE, IFICDB, IFIPAT, IFIUDB, NAPRALERT, PIRA, PROMT, TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
2523 REFERENCES IN FILE CA (1907 TO DATE)
20 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
2531 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:146002

REFERENCE 2: 140:127260

REFERENCE 3: 140:111411

REFERENCE 4: 140:108742

REFERENCE 5: 140:108579

REFERENCE 6: 140:106718

REFERENCE 7: 140:104477

REFERENCE 8: 140:104459

REFERENCE 9: 140:104246

REFERENCE 10: 140:94037

L51 ANSWER 14 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN
RN **9028-16-4** REGISTRY
CN Reductase, D-xylulose (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2,3-cis-Polyol dehydrogenase

CN D-Xylulose reductase
CN Dehydrogenase, 2,3-cis-polyol
CN E.C. 1.1.1.9
CN Erythritol dehydrogenase
CN NAD-dependent meso-erythritol dehydrogenase
CN **NAD-dependent xylitol dehydrogenase**
CN Polyol dehydrogenase
CN **Xylitol dehydrogenase**
DR 9032-74-0
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CASREACT, CIN, EMBASE, PIRA, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
213 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
214 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:127260

REFERENCE 2: 140:24162

REFERENCE 3: 140:14605

REFERENCE 4: 139:260078

REFERENCE 5: 139:260077

REFERENCE 6: 139:226997

REFERENCE 7: 139:225259

REFERENCE 8: 139:178733

REFERENCE 9: 139:176481

REFERENCE 10: 139:163668

=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 16:17:29 ON 04 MAR 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE LAST UPDATED: 3 Mar 2004 (20040303/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L49 ANSWER 1 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:486085 HCAPLUS
DN 139:225259
ED Entered STN: 26 Jun 2003
TI **DNA** microarray analysis of the expression of the **genes** encoding the major enzymes in ethanol production during glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast**
AU Sedlak, Miroslav; Edenberg, Howard J.; **Ho, Nancy W. Y.**
CS School of Engineering, Laboratory of Renewable Resources Engineering, Purdue University, West Lafayette, IN, 47907-2022, USA
SO Enzyme and Microbial Technology (2003), 33(1), 19-28
CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science
DT Journal
LA English
CC 3-3 (Biochemical **Genetics**)
Section cross-reference(s): 10, 16
AB Lignocellulosic biomass, which contains large amts. of glucose and xylose, is the new ideal feedstock for ethanol production used as renewable liquid fuel for transportation. The naturally occurring Saccharomyces **yeasts** traditionally used for industrial ethanol production are unable to ferment xylose. The authors have successfully developed genetically engineered Saccharomyces **yeasts** that can effectively co-ferment both glucose and xylose simultaneously to ethanol. The engineered **yeast** contains three xylose metabolizing **genes**, the **xylose reductase** (XR), **xylitol dehydrogenase** (XD) and **xylulokinase** (XK) **genes**, fused to glycolytic promoters, on high copy **plasmids** or integrated into the **yeast chromosome** in multiple copies. Although the glucose/xylose co-fermenting **yeasts** are currently the most effective **yeast** for producing ethanol from cellulosic biomass, they still utilize glucose more efficiently than xylose. The authors believe that carefully analyzing **gene** expression during co-fermentation of glucose and xylose to ethanol, using the genetically modified strains, will reveal ways to optimize xylose fermentation In this paper, the authors report the results on analyzing the expression of **genes** in the glycolytic and alc. fermentation pathways using microarray technol. The authors also report the results on the anal. of the activities of the selected enzymes for ethanol production during co-fermentation of glucose and xylose to ethanol by one of the effective glucose/xylose co-fermenting **yeasts** 424A(LNH-ST).
ST **DNA** microarray ethanol glucose xylose fermn Saccharomyces
IT **Saccharomyces cerevisiae**
(424A(LNH-ST); **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ADH1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ADH2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ADH3; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ADH4; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **DNA** microarray technology
(Affymetrix; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT Fermentation
Gene expression profiles, microbial
Genetic engineering
Glycolysis
(**DNA** microarray anal. of **genes** encoding enzymes
involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by
metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ENO1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(ENO2; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(FBI1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(GLK1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(GPM1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HXK1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)

(HXK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PDC1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PDC5; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PDC6; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PFK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PFK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PGI1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PGK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PYK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(PYK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TDH1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered Saccharomyces **yeast**

424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TDH2; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TDH3; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(TPI1; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT Enzymes, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(glycolytic; **DNA** microarray anal. of **genes** encoding
enzymes involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by metabolically engineered Saccharomyces **yeast**
424A(LNH-ST))
IT 64-17-5, Ethanol, biological studies 591-59-3 9001-04-1, Pyruvate
decarboxylase 9001-59-6, Pyruvate kinase 9001-83-6, Phosphoglycerate
kinase 9031-72-5, Alcohol dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**DNA** microarray anal. of **genes** encoding enzymes
involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by
metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))
IT 50-99-7, D-Glucose, biological studies 58-86-6, Xylose, biological
studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(**DNA** microarray anal. of **genes** encoding enzymes
involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by
metabolically engineered Saccharomyces **yeast** 424A(LNH-ST))
IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4, Xylulokinase 99775-25-4,
Xylose reductase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
(**DNA** microarray anal. of **genes** encoding enzymes
involved in glycolysis and alc. fermentation glucose and xylose
co-fermentation by
metabolically engineered Saccharomyces **yeast** 424A(LNH-ST)
containing)
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Bradford, M; Anal Chem 1976, V72, P248 HCAPLUS
(2) Ho, N; WO 97/42307 HCAPLUS
(3) Ho, N; US 08/148581 1998
(4) Ho, N; US 5789210 1998 HCAPLUS
(5) Ho, N; ACS Symposium Series 2000, V767, P142
(6) Ho, N; Advances in biochemical engineering/biotechnology 1999
(7) Ho, N; Appl Environ Microbiol 1998, V64, P1852 MEDLINE
(8) Kotter, P; Appl Microbiol Biotechnol 1993, V38, P776
(9) Li, R; A laboratory guide to RNA: isolation analysis, and synthesis 1996,
P43

(10) Maitra, P; J Biol Chem 1971, V246, P475 HCAPLUS
(11) Walfridsson, M; Appl Microbiol Biotechnol 1997, V48, P218 HCAPLUS

L49 ANSWER 2 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2003:282043 HCAPLUS
DN 138:302748
ED Entered STN: 11 Apr 2003
TI Manufacture of five-carbon sugars and sugar alcohols
IN Miasnikov, Andrei; Ojamo, Heikki; Povelainen, Mira; Gros, Hakan; Toivari, Mervi; Richard, Peter; Ruohonen, Laura; Koivuranta, Kari; Londesborough, John; Aristidou, Aristos; Penttila, Merja; Plazanet-Menut, Claire; Deutscher, Josef
PA Xyrofin Oy, Finland
SO U.S. Pat. Appl. Publ., 96 pp., Cont.-in-part of U.S. Ser. No. 488,581, abandoned.
CODEN: USXXCO
DT Patent
LA English
IC ICM C12P007-18
ICS C12N001-21; C12N001-18
NCL 435158000; 435252300; 435254200
CC 16-2 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**

FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003068791	A1	20030410	US 2001-908744	20010720 <--
	HU 72187	A2	19960328	HU 1995-1288	19931105 <--
	HU 219016	B	20010129		
	AT 184917	E	19991015	AT 1993-924615	19931105 <--
	ES 2139024	T3	20000201	ES 1993-924615	19931105 <--
	US 5631150	A	19970520	US 1995-368395	19950103 <--
	WO 2001053306	A2	20010726	WO 2001-FI51	20010122
	WO 2001053306	A3	20020418		

W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI	US 1992-973325	B2	19921105	<--
	US 1993-110672	B1	19930824	<--
	US 1995-368395	A1	19950103	<--
	US 1997-790585	A2	19970129	
	US 2000-488581	B2	20000121	
	WO 2001-FI51	A2	20010122	

AB The invention relates to the methods of manufacturing C5 sugars and sugar alcs. as well as other compds. derived from the pentose phosphate pathway from readily available substrates such as hexoses using metabolically engineered microbial hosts.
ST pentose pentitol fermn bacteria genetic engineering; **gene** sequence xylitol arabitol phosphate dehydrogenase
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(APDH; manufacture of five-carbon sugars and sugar alcs.)
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(DOG1; manufacture of five-carbon sugars and sugar alcs.)
IT **Gene**, microbial

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(LTP1; manufacture of five-carbon sugars and sugar alcs.)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(XPDH; manufacture of five-carbon sugars and sugar alcs.)

IT **DNA** sequences
Protein sequences
(bacterial xylitol and arabitol phospphate dehydrogenases)

IT Bacillus subtilis
Genetic engineering
Pentose phosphate pathway
Saccharomyces cerevisiae
(manufacture of five-carbon sugars and sugar alcs.)

IT Alditols
Pentoses
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(manufacture of five-carbon sugars and sugar alcs.)

IT Bacillus halodurans
Enterococcus avium
Lactobacillus rhamnosus
(manufacture of five-carbon sugars and sugar alcs. with enzyme from)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(rpi; manufacture of five-carbon sugars and sugar alcs.)

IT 510787-74-3 510787-76-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 9035-82-9, Dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(for arabitol phosphate; manufacture of five-carbon sugars and sugar alcs.)

IT 87-99-0P, Xylitol 488-81-3P, Ribitol 488-82-4P, D-Arabitol 488-84-6P, D-Ribulose 551-84-8P, D-Xylulose 1114-34-7P, D-Lyxose 6917-36-8P, Pentitol 10323-20-3P, D-Arabinose
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(manufacture of five-carbon sugars and sugar alcs.)

IT **9028-16-4**, **Xylitol dehydrogenase** 64886-68-6, Xylitol phosphate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(manufacture of five-carbon sugars and sugar alcs.)

IT 510787-75-4 510787-77-6
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 510944-98-6 510944-99-7 510945-00-3 510945-01-4 510945-02-5
510945-03-6 510945-04-7 510945-05-8 510945-06-9 510945-07-0
510945-08-1 510945-09-2 510945-10-5 510945-11-6 510945-12-7
510945-13-8 510945-14-9 510945-15-0 510945-16-1 510945-17-2
510945-18-3 510945-19-4 510945-20-7 510945-21-8 510945-23-0
510945-25-2 510945-26-3 510945-31-0 510945-32-1 510945-33-2
510945-34-3 510945-35-4 510945-36-5 510945-37-6 510945-38-7
510945-39-8 510945-40-1 510945-42-3 510945-43-4 510945-44-5
510945-45-6 510945-46-7 510945-47-8 510945-48-9 510945-49-0
510945-50-3 510945-51-4 510945-52-5 510945-53-6 510945-54-7
510945-55-8
RL: PRP (Properties)
(unclaimed nucleotide sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 510945-22-9 510945-24-1 510945-27-4 510945-28-5 510945-29-6
510945-30-9 510945-41-2
RL: PRP (Properties)

(unclaimed protein sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 351900-48-6 351900-49-7 351900-50-0 351900-51-1 351900-52-2
351900-53-3 351900-54-4 351900-55-5
RL: PRP (Properties)
(unclaimed sequence; manufacture of five-carbon sugars and sugar alcs.)

L49 ANSWER 3 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:545704 HCAPLUS
DN 135:136473
ED Entered STN: 27 Jul 2001
TI Manufacture of five-carbon sugars and sugar alcohols using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway
IN Miasnikov, Andrei; Ojamo, Heikki; Povelainen, Mira; Gros, Hakan; Toivari, Mervi; Richard, Peter; Ruohonen, Laura; Koivuranta, Kari; Londesborough, John; Aristidou, Aristos; Penttilae, Merja; Plazanet-Menut, Claire; Deutscher, Josef
PA Xyrofin Oy, Finland
SO PCT Int. Appl., 205 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07H
CC 16-2 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**, 6, 10, 33
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	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001053306	A2	20010726	WO 2001-FI51	20010122
	WO 2001053306	A3	20020418		
	W: AE, AG, AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, CZ, DE, DE, DK, DK, DM, DZ, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 2001031784	A5	20010731	AU 2001-31784	20010122
	BR 2001007918	A	20021105	BR 2001-7918	20010122
	EP 1254244	A2	20021106	EP 2001-903815	20010122
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	JP 2003520583	T2	20030708	JP 2001-553780	20010122
	US 2003068791	A1	20030410	US 2001-908744	20010720 <--
PRAI	US 2000-488581	A	20000121		
	US 1992-973325	B2	19921105 <--		
	US 1993-110672	B1	19930824 <--		
	US 1995-368395	A1	19950103 <--		
	US 1997-790585	A2	19970129		
	WO 2001-FI51	W	20010122		

AB The invention relates to the methods of manufacturing five-carbon sugars and sugar alcs. as well as other compds. derived from pentose-phosphate pathway (PPP) from readily available substrates such a hexoses using metabolically engineered microbial hosts. A series of the **genes** involved in the PPP are cloned from various microorganisms or disrupted in the host of either Bacillus subtilis or Saccharomyces cerevisiae. This strategy is demonstrated to successfully increase the yield of a variety of the five-carbon sugar or sugar alcs. for manufacturing purpose.
ST five carbon sugar alc fermn Bacillus Saccharomyces PPP **gene**;

pentose phosphate pathway **gene** mutagenesis overexpression transformation fermn

IT **Plasmid** vectors
(B1003, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B1011, **gene** IDP2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B1068, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B11154, **gene** XKS1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B1187, **gene** PGI1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B1449, **gene** LTP1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(B995, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Klebsiella terrigena
(D-xylulose-forming arabitol dehydrogenase **gene**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(DOG1, for 2-deoxyglucose-6-phosphate phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(DOG2, for 2-deoxyglucose-6-phosphate phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GDH2, expression in Pichia stipitis of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(LTP, for Low Mol. Weight Protein-Tyrosine Phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(LTP1, for Low Mol. Weight Protein-Tyrosine Phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or

transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)
(MAE1, overexpression and carbon source utilization in Saccharomyces cerevisiae; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Peptoniphilus asaccharolyticus
(NAD-glutamate dehydrogenase of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PFK26, for 6-phosphofructo-L-kinase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PFK27, for 6-phosphofructo-L-kinase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(PGI1, for phosphoglucoisomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(PPPase1; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(PPPase2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(TKL1; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(TKL2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Morganella morganii
(XDH (**xylitol dehydrogenase**) **gene** cloned from; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(XK, expression in Pichia stipitis of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(XYL1, for **xylose reductase**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(XYL2, for xylose dehydrogenase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Fermentation
(anaerobic; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Hexoses
Pentoses
Polysaccharides, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(as carbon source; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Redox reaction
(biochem., electron transport using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Brevibacterium
Corynebacterium
(fermentation host; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Pichia
Saccharomyces
Schizosaccharomyces
Schizosaccharomyces pombe
Yamadazyma
Yamadazyma stipitis
(fermentation using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Michaelis constant
(for nicotinamide coenzymes of malic enzyme of **yeast**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(fucI, for L-fucose isomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Ralstonia eutropha
(**genes** for polyhydroxybutyrate biosynthetic enzymes of, expression in **yeast** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Operon
(glcUgdh; manufacture of five-carbon sugars and sugar alcs. using

microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Biological transport
(glucose; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Carboxylic acids, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(hydroxy, polymers, fermentation of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Pseudomonas cichorii
(ketose 3-epimerase **gene** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Corynebacterium glutamicum
(lysine fermentation with transgenic; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Aspergillus nidulans
(malic enzyme of, expression in Pichia of **gene** for; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Bacillus halodurans
Bacillus subtilis
Biomass
Clostridium difficile
DNA sequences
Electron transport system, biological
Enterococcus avium
Fermentation
Lactobacillus rhamnosus
Molecular cloning
Mutagenesis
Pentose phosphate pathway
Protein sequences
Trichoderma reesei
Zygosaccharomyces rouxii
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Coenzymes
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(nicotinamide; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Enzyme kinetics

(of malic enzyme of Saccharomyces cerevisiae; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(p131, rpi **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(p131:Cm-2, rpi **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pAOS63, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pAOS64, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pAOS66, XYL1 and XYL2 **genes** on, expression in Pichia stipitis of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pAOS67, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pBS(AR2T), D-ribulose-5-phosphate epimerase **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pBS(AR2T)-kan, D-ribulose-5-phosphate epimerase **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pBS, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pGT21, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pGT23, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pGTK24(MXD2), **xylitol dehydrogenase gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pGTK24, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Plasmid** vectors
(pTKT:E1, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Glycolysis
(partial blocking through PPP enzymes; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Alcohols, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(polyhydric; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Saccharomyces cerevisiae**
(redox enzymes of, expression in Pichia of **genes** for; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Klebsiella pneumoniae
(ribitol dehydrogenase **gene** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(rpi, for D-ribose-phosphate isomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Carbohydrates, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(sugar phosphates; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(tkt, for transketolase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(tsr, or fba, for aldolase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT Zymomonas mobilis
(zwf **gene** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(zwf, in regulation of PPP oxidative capacity; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 311826-80-9 311826-82-1 351916-74-0 351916-75-1 351916-76-2 351916-79-5
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351916-81-9 351916-83-1
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(amino acid sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermentation of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 50-99-7, D-Glucose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(five carbon sugar or sugar alc. fermentation from; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 65187-56-6, 2-Deoxyglucose-6-phosphate phosphatase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**gene** DOG1; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 79747-53-8, Phosphatase, phosphoprotein (phosphotyrosine)
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**gene** PPPase1 or PPPase2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9001-46-1, NAD-dependent glutamate dehydrogenase
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(**gene** for, of Saccharomyces cerevisiae, cloning and expression of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9028-18-6, Arabitol dehydrogenase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**gene** for; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 60063-83-4, L-Fucose isomerase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(**gene** fucI; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9001-40-5, Glucose-6-phosphate dehydrogenase 9001-82-5, 6-Phosphogluconate dehydrogenase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(in regulation of PPP oxidative capacity; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9001-36-9, Glucokinase 9001-41-6, Phosphoglucoisomerase 9001-51-8, Hexokinase 37278-03-8, Phosphofructokinase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(in regulation of glucose uptake and glucose carbon flow into PPP; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 87-99-0P, Xylitol 488-81-3P, Ribitol 488-84-6P, D-Ribulose

551-84-8P, Xylulose 1114-34-7P, D-Lyxose 2152-56-9P, Arabitol
4151-19-3P, Ribulose-5-phosphate 4212-65-1P, Xylulose-5-phosphate
4300-28-1P, Ribose 5-phosphate 10323-20-3P, D-Arabinose
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 58-86-6P, Xylose, biological studies
RL: BMF (Bioindustrial manufacture); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 53-57-6, NADPH 53-59-8, NADP 53-84-9, NAD 58-68-4, NADH 64-69-7
9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 79082-92-1, Fructose-2,6-bisphosphate
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT **9030-58-4**, **Xylulokinase** 64886-68-6, Xylitol-phosphate dehydrogenase
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9001-80-3, Kinase (phosphorylating), phosphofructo- 9014-23-7, Ribitol dehydrogenase 9014-48-6, Transketolase 9023-83-0, Isomerase, ribose phosphate 9024-20-8, D-Ribulose 5-phosphate Epimerase **9028-16-4**, **Xylitol dehydrogenase** 9031-25-8, D-Mannose isomerase **99775-25-4**, **Xylose reductase** 150316-09-9, D-Ketohexose 3-epimerase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 6917-36-8P, Pentitol
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manufacture of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351916-80-8 351916-82-0
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351916-77-3 351916-78-4
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequences; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9024-52-6, Aldolase
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(promoter from the **gene** for; manufacture of five-carbon sugars and

sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9028-46-0, Malic enzyme 9028-86-8, Aldehyde dehydrogenase
104118-53-8, Xylose reductase
RL: BPR (Biological process); BSU (Biological study, unclassified); CAT (Catalyst use); BIOL (Biological study); PROC (Process); USES (Uses)
(redox system using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351919-59-0 351919-60-3 351919-61-4 351919-62-5 351919-63-6
351919-64-7 351919-65-8 351919-66-9 351919-67-0 351919-68-1
351919-69-2 351919-70-5 351919-71-6 351919-72-7 351919-73-8
351919-74-9 351919-75-0 351919-76-1 351919-77-2 351919-78-3
351919-79-4 351919-80-7 351919-81-8 351919-82-9 351919-83-0
351919-84-1 351919-85-2 351919-86-3 351919-87-4 351919-88-5
351919-89-6 351919-90-9 351919-91-0 351919-92-1 351919-93-2
351919-94-3 351919-95-4 351919-96-5 351919-98-7 351920-00-8
351920-01-9 351920-03-1 351920-04-2 351920-05-3 351920-06-4
351920-07-5 351920-08-6 351920-09-7 351920-10-0 351920-11-1, 1:
PN: WO0153306 SEQID: 1 unclaimed **DNA**
RL: PRP (Properties)
(unclaimed nucleotide sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351919-99-8
RL: PRP (Properties)
(unclaimed protein sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351900-48-6 351900-49-7 351900-50-0 351900-51-1 351900-52-2
351900-53-3 351900-54-4 351900-55-5
RL: PRP (Properties)
(unclaimed sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

L49 ANSWER 4 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:746143 HCAPLUS
DN 128:2978
ED Entered STN: 27 Nov 1997
TI Stable recombinant **yeasts** for fermenting xylose to ethanol
IN **Ho, Nancy W. Y.; Chen, Zheng-Dao**
PA Purdue Research Foundation, USA; Ho, Nancy W. Y.; Chen, Zheng-Dao
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N001-16
ICS C12N001-18; C12N001-19; C12N015-09; C12N015-68; C12N015-69; C12N015-81; C12P007-06
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9742307	A1	19971113	WO 1997-US7663	19970506 <--

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN,

ML, MR, NE, SN, TD, TG

AU 9728301	A1	19971126	AU 1997-28301	19970506	<--
AU 731102	B2	20010322			
EP 898616	A1	19990303	EP 1997-922698	19970506	<--
R: AT, BE, DE, DK, ES, FR, GB, GR, IT, NL, SE, PT, IE, FI					
CN 1225125	A	19990804	CN 1997-196195	19970506	<--
JP 2000509988	T2	20000808	JP 1997-540153	19970506	<--
BR 9710963	A	20010731	BR 1997-10963	19970506	<--
PRAI US 1996-16865P	P	19960506	<--		
WO 1997-US7663	W	19970506	<--		

AB Described are recombinant **yeast** which ferment xylose to EtOH and which maintain their ability to do so when cultured for numerous generations in non-selective media. The preferred **yeast** contain multiple copies of integrated **genes** encoding **xylose reductase**, **xylitol dehydrogenase**, and **xylulokinase** fused to promoters which are non-glucose inhibited and which do not require xylose for induction. Also described are preferred methods for integrating multiple copies of exogenous **DNA** into host cells by transforming cells with replicative/integrative vectors, and then replicating the cells a number of times under selective pressure to promote retention of the vector in subsequent generations. The replicated vectors thus serve to integrate multiple copies of the exogenous **DNA** into the host cells throughout the replication/selection phase. Thereafter the selective pressure can be removed to promote loss of the vector in subsequent generations, leaving stable integrants of the exogenous **DNA.**

ST Saccharomyces recombinant ethanol fermn xylose

IT Genetic engineering
Saccharomyces cerevisiae
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT **9028-16-4**, **Xylitol dehydrogenase**
9030-58-4, **Xylulokinase 99775-25-4**,
Xylose reductase
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT 58-86-6, D-Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(stable recombinant **yeasts** for fermenting xylose to ethanol)

L49 ANSWER 5 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:464186 HCAPLUS
DN 127:94156
ED Entered STN: 24 Jul 1997
TI Fermentation of corn fiber sugars by an engineered xylose utilizing Saccharomyces **yeast** strain
AU Moniruzzaman, M.; Dien, B.S.; Skory, C.D.; **Chen, Z.D.**; Hespell, R.B.; **Ho, N.W.Y.**; Dale, B.E.; Bothast, R.J.
CS Department of Chemical Engineering, Texas AandM University, College Station, TX, 77843, USA
SO World Journal of Microbiology & Biotechnology (1997), 13(3), 341-346
CODEN: WJMBEY; ISSN: 0959-3993
PB Rapid Science Publishers
DT Journal
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)

AB The ability of a recombinant Saccharomyces **yeast** strain to ferment the sugars glucose, xylose, arabinose and galactose which are the predominant monosaccharides found in corn fiber hydrolyzates has been examined Saccharomyces strain 1400 (pLNH32) was genetically engineered to ferment xylose by expressing **genes** encoding a **xylose reductase**, a **xylitol dehydrogenase** and a **xylulose kinase.** The recombinant efficiently fermented xylose alone or in the presence of glucose. Xylose-grown cultures had very little difference in xylitol accumulation, with only 4 to 5 g/L accumulating, in aerobic, micro-aerated and anaerobic conditions. Highest production of ethanol with all sugars was achieved under anaerobic conditions. From a mixture of glucose (80 g/L) and xylose (40 g/L), this strain produced 52 g/L ethanol, equivalent to 85% of theor. yield, in less than 24 h. Using a mixture of glucose (31 g/L), xylose (15.2 g/L), arabinose (10.5 g/L) and galactose (2 g/L), all of the sugars except arabinose were consumed in 24 h with an accumulation of 22 g ethanol/L, a 90% yield (excluding the arabinose in the calcn. since it is not fermented). Approx. 98% theor. yield, or 21 g ethanol/L, was achieved using an enzymic hydrolyzate of ammonia fiber exploded corn fiber containing an estimated 47.0 g mixed sugars/L.
In all mixed sugar fermns., less than 25% arabinose was consumed and converted into arabitol.

ST corn fiber sugar fermn Saccharomyces xylose; ethanol fermn corn fiber xylose **yeast**

IT Fermentation
(fermentation of corn fiber sugars by engineered xylose utilizing Saccharomyces **yeast** strain)

IT Carbohydrates, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(fermentation of corn fiber sugars by engineered xylose utilizing Saccharomyces **yeast** strain)

IT Corn
(fiber; fermentation of corn fiber sugars by engineered xylose utilizing Saccharomyces **yeast** strain)

IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(fermentation; fermentation of corn fiber sugars by engineered xylose utilizing Saccharomyces **yeast** strain)

IT 50-99-7, Glucose, biological studies 58-86-6, Xylose, biological studies 59-23-4, Galactose, biological studies 147-81-9, Arabinose
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(fermentation of corn fiber sugars by engineered xylose utilizing Saccharomyces **yeast** strain)

L49 ANSWER 6 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:671095 HCAPLUS
DN 126:2045
ED Entered STN: 13 Nov 1996
TI **Yeast** Sequencing Reports: Sequence and analysis of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus
AU Bolen, Paul L.; Hayman, G. Thomas; Shepherd, Hurley S.
CS Microbial Properties Res., National Center Agricultural Utilization Res., Agricultural Res. Serv., U.S. Dep. Agriculture, Peoria, IL, 61604, USA
SO Yeast (**1996**), 12(13), 1367-1375
CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
CC 3-3 (Biochemical **Genetics**)

Section cross-reference(s): 7, 10

AB A **xylose reductase gene** was isolated from the xylose-fermenting **yeast** Pachysolen tannophilus as a cDNA clone by selecting clones that hybridized specifically to xylose-inducible mRNA. Use of the cDNA clone as a probe in Northern hybridizations identified a xylose-inducible mRNA. Use of the cDNA clone as a probe in Northern hybridizations identified a xylose-inducible mRNA species large enough to encode a 36 kDa **xylose reductase** protein known to be produced by this **yeast.** A corresponding genomic clone was isolated as a 3 kb EcoRI fragment that specifically hybridized to the cDNA clone. The sequence of the cDNA and the largest open reading frame of the genomic clone are identical. The predicted translation product exhibits: (1) significant sequence identity with a previously published N-terminal amino acid sequence from purified P. tannophilus xylose (**aldose**) **reductase** protein exhibiting NADH/NADHP-dependent activities (**aldose reductase**, EC 1.1.1.21); (2) identity with a protein composed of 317 amino acid residues with a calculated mol. mass of 36·2 kDa, equivalent to that reported for purified P. tannophilus **xylose reductase**; and (3) considerable sequence similarity to, and features of, a superfamily of oxidoreductases. This sequence is deposited as GenBank Accession Number U40706.

ST **DNA** sequence Pachysolen **aldose reductase gene**; **aldose reductase** protein sequence Pachysolen

IT **DNA** sequences
Pachysolen tannophilus
Protein sequences
cDNA sequences
(sequence and anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus)

IT **183327-22-2**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus)

IT 58-86-6, Xylose, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus)

IT **183399-64-6**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(nucleotide sequence; anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus)

IT **9028-31-3, Aldose reductase**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(sequence and anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting **yeast** Pachysolen tannophilus)

L49 ANSWER 7 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:606013 HCAPLUS
DN 125:270220
ED Entered STN: 11 Oct 1996
TI A glycerol-3-phosphate dehydrogenase-deficient mutant of Saccharomyces cerevisiae expressing the heterologous XYL1 **gene**
AU Liden, G.; Walfridsson, M.; Ansell, R.; Anderlund, M.; Adler, L.;

Hahn-Haegerdal, B.
CS Dep. Chem. Reaction Eng., Chalmers Univ. Technol., Goeteborg, S-412 96, Swed.
SO Applied and Environmental Microbiology (**1996**), 62(10), 3894-3896
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
CC 10-4 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): **3**
AB The **gene** XYL1, encoding a **xylose reductase**, from Pichia stipitis was transformed into a mutant of Saccharomyces cerevisiae incapable of glycerol production because of deletion of the **genes** GPD1 and GPD2. The transformed strain was capable of anaerobic glucose conversion in the presence of added xylose, indicating that the **xylose reductase** reaction can fulfill the role of the glycerol-3-phosphate dehydrogenase reaction as a redox sink. The specific xylitol production rate obtained was 0.38 g g-1 h-1.
ST Pichia **xylose reductase gene** cloning Saccharomyces; **yeast gene** XYL1 cloning glycerol dehydrogenase
IT Molecular cloning
Saccharomyces cerevisiae
Yamadazyma stipitis
(glycerol-3-phosphate dehydrogenase-deficient mutant of Saccharomyces cerevisiae expressing heterologous XYL1 **gene**)
IT **Gene**, microbial
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(XYL1, glycerol-3-phosphate dehydrogenase-deficient mutant of Saccharomyces cerevisiae expressing heterologous XYL1 **gene**)
IT 9075-65-4, Glycerol-3-phosphate dehydrogenase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(glycerol-3-phosphate dehydrogenase-deficient mutant of Saccharomyces cerevisiae expressing heterologous XYL1 **gene**)
IT **95829-40-6, Xylose reductase**
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(glycerol-3-phosphate dehydrogenase-deficient mutant of Saccharomyces cerevisiae expressing heterologous XYL1 **gene**)

L49 ANSWER 8 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1996:308481 HCAPLUS
DN 124:340999
ED Entered STN: 25 May 1996
TI A metabolic engineering view on molecular breeding of an alcohol fermenting **yeast** from xylose
AU Seki, Tatsuji; Tantirungkij, Manee; Fujiyama, Kazuhito; Yoshida, Toshiomi
CS International Center Cooperative Research Biotechnology, Osaka University, Suita, 565, Japan
SO Environmental Biotechnology: Principles and Applications, [Papers presented at the International Symposium on Environmental Biotechnology], Waterloo, Ont., July 4-8, 1994 (**1996**), Meeting Date 1994, 114-124. Editor(s): Moo-Young, Murray; Anderson, William A.; Chakrabarty, Ananda M. Publisher: Kluwer, Dordrecht, Neth.
CODEN: 62UGA4
DT Conference
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**
AB Xylose-assimilating S. cerevisiae was constructed by introducing the **xylose reductase** and **xylitol dehydrogenase genes** originating from P. stipitis. Good

growth of the transformant in xylose medium was observed under aerobic conditions. Under a limited oxygen condition, the transformant produced a lesser amount of ethanol than P. stipitis, and a remarkable amount of xylitol was accumulated. A mutant, IM2, in which the ratio of **xylose reductase** to **xylitol dehydrogenase** activities was lower than the parental strain, exhibited an improved fermentation with less accumulation of xylitol and a higher yield. The limited feeding of xylose could also improve the fermentation, with reduced xylitol accumulation as well as increased ethanol yield. The facts suggest strongly that the path of the conversion from xylitol to xylulose is the "bottleneck" due to a poor regeneration of NAD essential for the conversion. An appropriate oxygen supply also improved the ethanol production and the production rate, suggesting it may contribute to the NAD recycle from NADH.

ST ethanol manuf Saccharomyces xylose

IT Fermentation
Genetic engineering
Saccharomyces cerevisiae
(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 58-86-6, Xylose, biological studies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 87-99-0P, Xylitol
RL: BYP (Byproduct); PREP (Preparation)
(genetic engineering of **yeast** for ethanol fermentation from xylose)

L49 ANSWER 9 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1996:158446 HCAPLUS

DN 124:252209

ED Entered STN: 19 Mar 1996

TI Sequencing and analysis of 51 kb on the right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames

AU Wieman, Stefan; Rechmann, Stefanie; Benes, Vladimir; Voss, Hartmut; Schwager, Christian; Vlcek, Cestmir; Stegemann, Josef; Zimmermann, Jurgen; Erfle, Holger; et al.

CS EMBL, Heidelberg, D-69117, Germany

SO Yeast (**1996**), 12(3), 281-8
CODEN: YESTE3; ISSN: 0749-503X

PB Wiley

DT Journal

LA English

CC 3-3 (Biochemical **Genetics**)

AB We have sequenced a region of 51 kb of the right arm from **chromosome** XV of Saccharomyces cerevisiae. The sequence contains 30 open reading frames (ORFs) of more than 100 amino acid residues. Thirteen new **genes** have been identified. Thirteen ORFs correspond to known **yeast genes.** One delta element and one tRNA **gene** were identified. Upstream of the RPO31 **gene**, encoding the largest subunit of RNA polymerase III, lies a Abflp binding site. The nucleotide sequence data reported in this paper are available in the EMBL, GenBank and DDBJ nucleotide sequence databases under the Accession Number X90518.

ST Saccharomyces **chromosome** XV **gene** sequence

IT Deoxyribonucleic acid sequences
Protein sequences
Saccharomyces cerevisiae
(sequencing and anal. of 51 kb on right arm of **chromosome** XV

from Saccharomyces cerevisiae reveals 30 open reading frames)
IT **Gene**, microbial
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT **Chromosome**
(Saccharomyces cerevisiae XV, sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT Ribonucleic acids, transfer
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(aspartic acid-specific, **gene** for; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT Protein formation elongation factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(eEF-2, **gene** for; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT 9014-24-8
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(III, **gene** for; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT **121548-71-8**, Protein (Saccharomyces cerevisiae **gene** GCY reduced) 122178-43-2, Profilin (Saccharomyces cerevisiae **gene** PFY) 133758-72-2 146313-69-1, Protein formation elongation factor EF 2 (Saccharomyces cerevisiae strain YM213 **gene** EFT1 reduced)
156656-75-6 157712-16-8 159521-43-4 172929-93-0 172929-97-4
174763-93-0 174763-94-1 174763-95-2 174763-96-3 174763-97-4
174763-98-5 174763-99-6 174764-00-2 174764-01-3 174764-02-4
174764-03-5 174764-04-6 174764-05-7 174764-06-8
RL: PRP (Properties)
(amino acid sequence; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT 86480-67-3
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**gene** for; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)
IT 170321-17-2, GenBank X90518
RL: PRP (Properties)
(nucleotide sequence; sequencing and anal. of 51 kb on right arm of **chromosome** XV from Saccharomyces cerevisiae reveals 30 open reading frames)

L49 ANSWER 10 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:814692 HCAPLUS
DN 124:2028
ED Entered STN: 27 Sep 1995
TI Isolation and characterization of the **gene** encoding **xylose reductase** from Kluyveromyces lactis
AU Billard, Patrick; Menart, Sandrine; Fleer, Reinhard; Bolotin-Fukuhara, Monique
CS Institut de Genetique et Microbiologie, Bat. 400, Universite Paris-Sud, 91405, Orsay, Fr.
SO Gene (**1995**), 162(1), 93-7
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
CC 3-3 (Biochemical **Genetics**)

Section cross-reference(s): 7, 10

AB The identification of a **xylose reductase** (XR)-encoding **gene** (XYL1) from the xylose-assimilating **yeast** Kluyveromyces lactis (Kl) is described. XYL1 was isolated as a highly expressed fusion clone from a 'lacZ translational fusion library. **DNA** sequence anal. revealed an open reading frame (ORF) of 987bp capable of encoding a polypeptide of 329 amino acids (aa). The deduced aa sequence displays a 62% overall identity to that of XR from Pichia stipitis. **Gene** disruption studies indicate that XYL1 exists as a single copy in the **yeast** genome and is essential for growth on xylose. Northern blot anal. of the XYL1 transcript and measurement of the XR enzymic activities show, in contrast to other known XR-encoding **genes**, a constitutive expression of Kl XYL1.

ST Kluyveromyces **xylose reductase gene** sequence; XYL1 **gene** Kluyveromyces **xylose reductase** sequence

IT Kluyveromyces lactis
(isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT Deoxyribonucleic acid sequences
(of **gene** XYL1 from Kluyveromyces lactis)

IT Protein sequences
(of **xylose reductase** from Kluyveromyces lactis)

IT **Gene**, microbial
RL: PRP (Properties)
(XYL1, isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT 171043-09-7
RL: PRP (Properties)
(amino acid sequence; isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT 58-86-6, Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT **104118-53-8, Xylose reductase**
RL: PRP (Properties)
(isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT 158764-02-4, GenBank L36993
RL: PRP (Properties)
(nucleotide sequence; isolation and characterization of **gene** encoding **xylose reductase** from Kluyveromyces lactis)

IT 53-57-6, NADPH
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**xylose reductase** from Kluyveromyces lactis dependence on NADPH)

L49 ANSWER 11 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:756362 HCAPLUS
DN 123:196764
ED Entered STN: 25 Aug 1995
TI Recombinant **yeasts** for effective fermentation of glucose and xylose
IN **Ho, Nancy W. Y.**; Tsao, George T.
PA Purdue Research Foundation, USA
SO PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DT Patent

LA English
IC ICM C12N001-14
ICS C12N009-00; C12N009-12; C12N015-00; C12P007-08
CC 16-5 (Fermentation and Bioindustrial Chemistry)
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9513362	A1	19950518	WO 1994-US12861	19941108	<--
	W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, UZ, VN					
	RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG					
	US 5789210	A	19980804	US 1993-148581	19931108	<--
	CA 2176038	AA	19950518	CA 1994-2176038	19941108	<--
	AU 9510517	A1	19950529	AU 1995-10517	19941108	<--
	AU 695930	B2	19980827			
	EP 728192	A1	19960828	EP 1995-901176	19941108	<--
	R: AT, BE, DE, DK, ES, FR, GB, GR, IE, IT, NL, SE					
	BR 9408010	A	19961217	BR 1994-8010	19941108	<--
	CN 1141057	A	19970122	CN 1994-194767	19941108	<--
	CN 1128873	B	20031126			
	JP 09505469	T2	19970603	JP 1994-513948	19941108	<--
	PL 176399	B1	19990531	PL 1994-314297	19941108	<--
	FI 9601926	A	19960704	FI 1996-1926	19960507	<--
PRAI	US 1993-148581	A	19931108	<--		
	US 1993-148541	A	19931108	<--		
	WO 1994-US12861	W	19941108	<--		

AB Described are recombinant **yeasts** containing **genes** encoding **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase**, and **DNA** mols., vectors and methods useful for producing such **yeasts.** The recombinant **yeasts** effectively ferment xylose to EtOH, and preferred **yeasts** are capable of simultaneously fermenting glucose and xylose to EtOH, thereby taking full advantage of these 2 sugar sources as they are found in agricultural biomass.

ST recombinant **yeast** ethanol fermn glucose xylose

IT Deoxyribonucleic acid sequences
(for **xylulokinase gene** of Saccharomyces cerevisiae)

IT Protein sequences
(for **xylulokinase** of Saccharomyces cerevisiae)

IT Fermentation
Saccharomyces cerevisiae
(recombinant **yeasts** for effective fermentation of glucose and xylose)

IT **Gene**, microbial
RL: PRP (Properties)
(**xylulokinase**; sequence of **xylulokinase gene** of Saccharomyces cerevisiae)

IT **167078-89-9**
RL: PRP (Properties)
(amino acid sequence; recombinant **yeasts** for effective fermentation of glucose and xylose)

IT **167974-35-8**
RL: PRP (Properties)
(nucleotide sequence; recombinant **yeasts** for effective fermentation of glucose and xylose)

IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4, Xylulokinase 99775-25-4, Xylose reductase
RL: CAT (Catalyst use); USES (Uses)
(recombinant **yeasts** containing cloned enzyme **genes** for

effective fermentation of glucose and xylose)
IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(recombinant **yeasts** for effective fermentation of glucose and xylose)
IT 50-99-7, Glucose, biological studies 58-86-6, Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)
(recombinant **yeasts** for effective fermentation of glucose and xylose)

L49 ANSWER 12 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:650857 HCAPLUS
DN 121:250857
ED Entered STN: 26 Nov 1994
TI Utilization of xylose with recombinant Saccharomyces cerevisiae harboring **genes** for xylose metabolism from Pichia stipitis
AU Meinander, Nina; Hallborn, Johan; Keranen, Sirkka; Ojamo, Heikki; Penttila, Merja; Walfridsson, Mats; Hahn-Haegerdal, Barbel
CS Chemical center, University Lund, Lund, S-22100, Swed.
SO Progress in Biotechnology (**1994**), 9(ECB6: PROCEEDINGS OF THE 6TH EUROPEAN CONGRESS ON BIOTECHNOLOGY, 1993, PT. 2), 1143-6
CODEN: PBITE3; ISSN: 0921-0423
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): **3**
AB Normally, S. cerevisiae lacks the enzymes necessary to convert xylose into xylulose and is thereby unable to utilize xylose in its metabolism An S. cerevisiae strain expressing both the **xylose reductase** (converting xylose to xylitol) and **xylitol dehydrogenase** (converting xylitol to xylulose) **genes** of P. stipitis was constructed. This strain was able to grow on and ferment xylose.
ST xylose metab Saccharomyces recombinant
IT Molecular cloning
Pichia stipitis
Saccharomyces cerevisiae
(xylose utilization by recombinant Saccharomyces cerevisiae harboring **genes** for xylose metabolism from Pichia stipitis)
IT **Gene**, microbial
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(xylose utilization by recombinant Saccharomyces cerevisiae harboring **genes** for xylose metabolism from Pichia stipitis)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(xylose utilization by recombinant Saccharomyces cerevisiae harboring **genes** for xylose metabolism from Pichia stipitis)
IT 58-86-6, Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(xylose utilization by recombinant Saccharomyces cerevisiae harboring **genes** for xylose metabolism from Pichia stipitis)

L49 ANSWER 13 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1994:650854 HCAPLUS
DN 121:250854
ED Entered STN: 26 Nov 1994
TI Bioconversion of xylose to xylitol with in situ generation of NAD(P)H in

recombinant Saccharomyces cerevisiae
AU Carlsen, Helle N.; Hallborn, Johan; Gorwa, Marie-Francoise; Hahn-Haegerdal, Baerbel
CS Chemical Center, University Lund, Lund, S-221 00, Swed.
SO Progress in Biotechnology (**1994**), 9(ECB6: PROCEEDINGS OF THE 6TH EUROPEAN CONGRESS ON BIOTECHNOLOGY, 1993, PT. 1), 313-16
CODEN: PBITE3; ISSN: 0921-0423
DT Journal
LA English
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): **3**
AB The **xylose reductase gene** of Pichia stipitis was cloned into S. cerevisiae. The recombinant S. cerevisiae was thus able to convert xylose to xylitol. The cofactor NAD(P)H, used for xylose reduction, could be generated in situ through the oxidation of ethanol, acetate, or glucose.
ST xylose metab Saccharomyces recombinant
IT Molecular cloning
Saccharomyces cerevisiae
(bioconversion of xylose to xylitol with in situ generation of NAD(P)H in recombinant Saccharomyces cerevisiae)
IT 58-86-6, Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(bioconversion of xylose to xylitol with in situ generation of NAD(P)H in recombinant Saccharomyces cerevisiae)
IT 53-57-6, NADPH 58-68-4, NADH
RL: BPR (Biological process); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative); PROC (Process)
(bioconversion of xylose to xylitol with in situ generation of NAD(P)H in recombinant Saccharomyces cerevisiae)
IT 87-99-0, Xylitol
RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
(bioconversion of xylose to xylitol with in situ generation of NAD(P)H in recombinant Saccharomyces cerevisiae)

L49 ANSWER 14 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN **1994:532375** HCAPLUS
DN **121:132375**
ED Entered STN: 17 Sep 1994
TI Manufacture of xylitol from carbon sources other than xylose or xylulose using **yeasts** expressing foreign **genes**
IN Harkki, Anu Marjukka; Myasnikov, Andrey Novomirovich; Apajalahti, Juha Heikki Antero; Pastinen, Ossi Antero
PA Xyrofin Oy, Finland
SO PCT Int. Appl., 90 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12P007-18
ICS C12N015-52
CC 16-2 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): 10, 17
FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9410325	A1	19940511	WO 1993-FI450	19931105 <--

W: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
AU 9454215 A1 19940524 AU 1994-54215 19931105 <--
EP 672161 A1 19950920 EP 1993-924615 19931105 <--
EP 672161 B1 19990922
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE
HU 72187 A2 19960328 HU 1995-1288 19931105 <--
HU 219016 B 20010129
JP 08505522 T2 19960618 JP 1994-510748 19931105 <--
JP 3433295 B2 20030804
BR 9307391 A 19990831 BR 1993-7391 19931105 <--
AT 184917 E 19991015 AT 1993-924615 19931105 <--
RU 2142999 C1 19991220 RU 1995-113172 19931105 <--
ES 2139024 T3 20000201 ES 1993-924615 19931105 <--
PL 178040 B1 20000229 PL 1993-308742 19931105 <--
FI 9502148 A 19950704 FI 1995-2148 19950504 <--
NO 9501747 A 19950705 NO 1995-1747 19950504 <--
PRAI US 1992-973325 A 19921105 <--
US 1993-110672 19930824 <--
WO 1993-FI450 W 19931105 <--

AB Novel methods for the fermentation of xylitol from sugars using a **yeast** with modified D-arabitol metabolism are described. **Yeasts** synthesizing D-arabitol were modified by the introduction of expression cassettes for D-arabitol dehydrogenase and **xylitol dehydrogenase** and by inactivation of the host **genes** for transketolase and D-**xylulokinase** and increasing levels of expression of **genes** for enzymes of the oxidative branch of the pentose phosphate pathway. **Plasmid** pSRT(AX)-9 carrying expression cassettes for D-arabitol dehydrogenase and **xylitol dehydrogenase** was introduced into Zygosaccharomyces rouxii. Transformants showing significant activities of the 2 enzymes were used to manufacture xylitol with yields of 7.7 g/L obtained after 48 h. Yields depended upon nutritional conditions with higher yields coming from a medium enriched with **yeast** extract

ST xylitol fermn transgenic **yeast**; arabitol metab xylitol fermn **yeast**; pentose phosphate pathway xylitol fermn **yeast**

IT **Gene**, microbial
RL: BIOL (Biological study)
(XYL2, for **xylitol dehydrogenase** of Pichia stipitis, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)

IT **Gene**, microbial
RL: BIOL (Biological study)
(for transketolase of Saccharomyces cerevisiae, cloning and inactivation of, xylitol manufacture in relation to)

IT **Gene**, microbial
RL: BIOL (Biological study)
(for D-arabitol dehydrogenase of Klebsiella terrigena, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)

IT Pentose phosphate pathway
(oxidative branch of, increasing activity of, in xylitol manufacture with fungi with altered arabitol metabolism)

IT **Plasmid** and Episome
(pCPU(AX), **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, expression in Candida polymorpha of, altered arabitol metabolism and xylitol manufacture in relation to)

IT **Plasmid** and Episome
(pSRT(AX)-9, **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, expression in

Zygosaccharomyces rouxii of, altered arabitol metabolism and xylitol manufacture
in relation to)
IT **Plasmid** and Episome
(pSRT(ZG), **genes** for D-glucose-6-phosphate dehydrogenase and 6-phospho-D-gluconate dehydrogenase on, expression in Zygosaccharomyces rouxii of)
IT **Plasmid** and Episome
(pTC(AX), integrating dominant selection vector for Torulopsis candida, **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, altered arabitol metabolism and xylitol manufacture in relation to)
IT Candida diddensii
Dendryphiella salina
Fungi
Pichia farinosa
Saccharomyces rouxii
Schizophyllum commune
Torulaspora hansenii
Torulopsis candida
Yeast
(xylitol manufacture with, with altered arabitol metabolism)
IT Fermentation
(xylitol, with transgenic fungi with altered arabitol metabolism)
IT Klebsiella terrigena
(D-arabitol dehydrogenase **gene** of, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)
IT **Gene**, microbial
RL: BIOL (Biological study)
(URA3, of Candida polymorpha, cloning of, transformation vectors for C. polymorpha and xylitol manufacture in relation to)
IT **Gene**, microbial
RL: BIOL (Biological study)
(gnd, of Escherichia coli, cloning of, alteration of pentose phosphate pathway in xylitol manufacture in relation to)
IT **Gene**, microbial
RL: BIOL (Biological study)
(zwf, of Saccharomyces cerevisiae, cloning of, alteration of pentose phosphate pathway in xylitol manufacture in relation to)
IT 87-99-0, Xylitol
RL: BIOL (Biological study)
(fermentation of, with transgenic **yeast**, modified arabitol metabolism and pentose phosphate pathway in)
IT 9001-40-5, D-Glucose-6-phosphate dehydrogenase 9024-20-8, D-Ribulose-5-phosphate-3-epimerase 9026-40-8, D-Ribulokinase 9073-95-4, 6-Phospho-D-gluconate dehydrogenase
RL: BIOL (Biological study)
(**gene** for, expression of, in fungal hosts with altered arabitol metabolism for manufacture of xylitol)
IT **9028-16-4**, **Xylitol dehydrogenase** 9028-18-6, D-Arabitol dehydrogenase
RL: BIOL (Biological study)
(**gene** for, expression of, in transgenic **yeast**, alteration of arabitol metabolism in xylitol manufacture in relation to)
IT 9014-48-6, Transketolase **9030-58-4**, D-**Xylulokinase**
RL: BIOL (Biological study)
(**gene** for, inactivation of, in fungal hosts with altered arabitol metabolism for manufacture of xylitol)
IT 2152-56-9, Arabitol
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, alteration of, in manufacture of xylitol with transgenic

yeasts)

L49 ANSWER 15 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:510092 HCAPLUS
DN 119:110092
ED Entered STN: 18 Sep 1993
TI Cloning and improveing the expression of Pichia stipitis **xylose reductase gene** in Saccharomyces cerevisiae
AU **Chen, Zhengdao**; **Ho, Nancy W. Y.**
CS Lab. Renewable Resourc. Eng., Purdue Univ., West Lafayette, IN, 47907-1295, USA
SO Applied Biochemistry and Biotechnology (**1993**), 39-40, 135-47
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 3-2 (Biochemical **Genetics**)
Section cross-reference(s): 16
AB The intact Pichia stipitis **xylose reductase gene** (XR) has been cloned and expressed in Saccharomyces cerevisiae. The possible further improvement of the expression of the Pichia **gene** in the new host was studied. To improve the expression of the XR **gene** in **yeast** (Saccharomyces cerevisiae), its 5'-noncoding sequence containing the genetic elements for transcription and translation was systematically replaced by that from the **yeast genes.** It was found that the Pichia genetic signal for transcription of XR is more effective than the **yeast** TRP5 promoter, but is about half as effective as the **yeast** strong promoter of the alc. dehydrogenase **gene** (ADC1). However, the nucleotide sequence immediately adjacent to the initiation codon of XR, which controls the translation of the **gene** product, seemed to be five times less effective than the corresponding sequence of the ADC1 **gene.** By totally replacing its 5'-noncoding sequence with that of the **yeast** ADC1 **gene**, the expression of XR in **yeast** was nearly ten times higher. Furthermore, the cloned Pichia XR described in this article contains very little of its 3'-noncoding sequence. In order to study whether the 3'-noncoding sequence is important to its expression in S. cerevisiae, the intact 3'-noncoding sequences of the **yeast xylulokinase gene** was spliced to the 3' end of the PADC1-XR structural **gene.** This latter modification has resulted in a 2-fold further increase in the expression of the Pichia XR in **yeast.**
ST Pichia **xylose reductase gene** cloning Saccharomyces
IT **Saccharomyces cerevisiae**
(cloning and expression in, of **xylose reductase gene** of Pichia stipitis)
IT **Gene**, microbial
RL: BIOL (Biological study)
(for **xylose reductase**, of Pichia stipitis, cloning and expression in Saccharomyces cerevisiae of)
IT Molecular cloning
(of **xylose reductase gene**, of Pichia stipitis, in Saccharomyces cerevisiae)
IT Pichia stipitis
(**xylose reductase gene** of, cloning and expression of, in Saccharomyces cerevisiae)
IT **95829-40-6**, **Xylose reductase**
RL: BIOL (Biological study)
(**gene** for, of Pichia stipitis, cloning and expression of, in Saccharomyces cerevisiae)

L49 ANSWER 16 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:226769 HCAPLUS

DN 118:226769
ED Entered STN: 12 Jun 1993
TI Isolation of **xylose reductase gene** of Pichia stipitis and its expression in Saccharomyces cerevisiae
AU Takuma, Shinya; Nakashima, Noriyuki; Tantirungkij, Manee; Kinoshita, Shinichi; Okada, Hirosuke; Seki, Tatsuji; Yoshida, Toshiomi
CS Fac. Eng., Osaka Univ., Suita, 565, Japan
SO Applied Biochemistry and Biotechnology (**1991**), 28-29, 327-40
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 3-2 (Biochemical **Genetics**)
Section cross-reference(s): 7, 10
AB A NADPH/NADH-dependent **xylose reductase gene** was isolated from the xylose-assimilating **yeast**, Pichia stipits. **DNA** sequence anal. showed that the **gene** consists of 951 bp. The **gene** introduced in Saccharomyces cerevisiae was transcribed to mRNA, and a considerable amount of enzyme activity was observed constitutively, whereas transcription and translation in P. stipitis were inducible. S. cerevisiae carrying the **xylose reductase gene** could not, however, grow on xylose medium, and could not produce ethanol from xylose. Since xylose uptake and accumulation of xylitol by S. cerevisiae were observed, the conversion of xylitol to xylulose seemed to be limited.
ST Pichia **xylose reductase gene** cloning sequence; Saccharomyces cloning **xylose reductase gene** Pichia
IT **Saccharomyces cerevisiae**
(cloning and expression in, of **xylose reductase gene**, of Pichia stipitis)
IT **Gene**, microbial
RL: BIOL (Biological study)
(for **xylose reductase**, of Pichia stipitis, cloning and expression and sequencing of)
IT Deoxyribonucleic acid sequences
(of **xylose reductase gene**, of Pichia stipitis)
IT Molecular cloning
(of **xylose reductase gene**, of Pichia stipitis, for expression in **yeast**)
IT Protein sequences
(of **xylose reductase**, of Pichia stipitis)
IT Pichia stipitis
(**xylose reductase gene** of, sequence and expression in **yeast** of)
IT **138263-97-5**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)
IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(**gene** for, of Pichia stipitis, cloning and expression and sequencing of)
IT 147651-00-1
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L49 ANSWER 17 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:190040 HCAPLUS
DN 118:190040
ED Entered STN: 14 May 1993
TI Secretion of a xylanase from Cryptococcus albidus by Saccharomyces cerevisiae and Pichia stipitis

AU Morosoli, Rolf; Zalce, Eugenia; Moreau, Alain; Durand, Serge
CS Cent. Rech. Microbiol. Appl., Inst. Armand-Frappier, Ville de Laval, QC, H7N 4Z3, Can.
SO Progress in Biotechnology (**1992**), 7(Xylans Xylanases), 247-58
CODEN: PBITE3; ISSN: 0921-0423
DT Journal
LA English
CC 16-4 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**
AB The xylanase **gene** of Cryptococcus albidus and its cDNA were each inserted in the vector pVT100 and in the vector pJHS to transform Saccharomyces cerevisiae and Pichia stipitis, resp. The xylanase **gene** was under the control of its own promoter for expts. in S. cerevisiae, while in P. stipitis it was under the control of the **xylose reductase** promoter of the same strain. **Yeasts** transformed with **plasmids** containing the cDNA of the structural xylanase **gene** produced active extracellular xylanase. The enzyme secreted by S. cerevisiae had an apparent mol. mass of 48-kDa, which corresponds to that of the native xylanase produced by C. albidus. The enzyme synthesized by P. stipitis, however, had an apparent mol. mass of 50-kDa, probably reflecting a different protein glycosylation level by this strain. With **plasmids** bearing the genomic xylanase **gene**, transcription occurred, but the seven introns interrupting the xylanase **gene** were neither spliced out by S. cerevisiae nor by P. stipitis and no enzyme was produced. Expression of the xylanase **gene** by P. stipitis, resulted in a **yeast** able to grow on xylan as carbon source, directly fermenting it to ethanol under anaerobic conditions.
ST Cryptococcus xylanase **gene** cloning Saccharomyces Pichia
IT Pichia stipitis
Saccharomyces cerevisiae
(cloning and expression in, of xylanase **gene** of Cryptococcus albidus)
IT **Gene**, microbial
RL: BIOL (Biological study)
(for xylanase, of Streptococcus albidus, cloning and expression in Saccharomyces cerevisiae and Pichia stipitis of)
IT Molecular cloning
(of xylanase **gene**, of Cryptococcus albidus, in Saccharomyces cerevisiae and Pichia stipitis)
IT Cryptococcus albidus
(xylanase **gene** of, cloning and expression of, in Saccharomyces cerevisiae and Pichia stipitis)
IT 37278-89-0, Xylanase
RL: BIOL (Biological study)
(**gene** for, of Cryptococcus albidus, cloning and expression in Saccharomyces cerevisiae and Pichia stipitis of)

L49 ANSWER 18 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:123016 HCAPLUS
DN 118:123016
ED Entered STN: 30 Mar 1993
TI Xylitol production by recombinant Saccharomyces cerevisiae
AU Hallborn, Johan; Walfridsson, Mats; Airaksinen, Ulla; Ojamo, Heikki; Hahn-Hagerdal, Barbel; Penttila, Merja; Keranen, Sirkka
CS VTT Biotech. Lab., Espoo, SF-02151, Finland
SO Bio/Technology (**1991**), 9(11), 1090-5
CODEN: BTCHDA; ISSN: 0733-222X
DT Journal
LA English
CC 16-2 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**, 7, 10
AB Efficient conversion of xylose to xylitol was obtained by transforming

Saccharomyces cerevisiae with the **gene** encoding the **xylose reductase** (XR) of Pichia stipitis CBS 6054. Comparison of the **chromosomal** and cDNA copies of the XYL1 **gene** showed that the genomic XYL1 contains no introns, and an XR monomer of 318 amino acids (35,985 Da) is encoded by an open reading frame of 954 bp. The amino acid sequence of the P. stipitis XR is similar to several **aldose reductases**, suggesting that P. stipitis XR is part of the aldoketo reductase superfamily. S. cerevisiae transformed with the XYL1 **gene** gave over 95% conversion of xylose into xylitol, a yield not obtainable with natural xylose utilizing **yeasts.**

ST xylitol fermn xylose recombinant Saccharomyces; **xylose reductase gene** XYL1 sequence Pichia

IT **Saccharomyces cerevisiae**
(cloning and expression in, of **xylose reductase gene** of Pichia stipitis)

IT Molecular cloning
(of **xylose reductase gene**, of Pichia stipitis, in Saccharomyces cerevisiae)

IT Protein sequences
(of **xylose reductase**, of Pichia stipitis)

IT Fermentation
(xylitol, from xylose by recombinant Saccharomyces cerevisiae)

IT Pichia stipitis
(**xylose reductase** of, **gene** for, cloning and sequence of)

IT Deoxyribonucleic acid sequences
(complementary, for **xylose reductase** of Pichia stipitis)

IT **Gene**, microbial
RL: BIOL (Biological study)
(XYL1, for **xylose reductase**, of Pichia stipitis, cloning and sequence of)

IT **138263-97-5**, **Xylose reductase** (Pichia stipitis reduced)
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

IT **95829-40-6**, **Xylose reductase**
RL: BIOL (Biological study)
(**gene** for, of Pichia stipitis, cloning and sequence of)

IT 87-99-0P, Xylitol
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manufacture of, from xylose by recombinant Saccharomyces cerevisiae)

IT **146409-21-4**
RL: PRP (Properties)
(nucleotide sequence of)

IT **146409-22-5**
RL: PRP (Properties)
(nucleotide sequence of, complete)

IT 58-86-6, D-Xylose, uses
RL: USES (Uses)
(xylitol manufacture from, by recombinant Saccharomyces cerevisiae)

L49 ANSWER 19 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN **1993:100558** HCAPLUS
DN **118:100558**
ED Entered STN: 19 Mar 1993
TI Xylitol manufacture with **yeast** mutants
IN Apajalahti, Juha; Leisola, Matti
PA Xyrofin Oy, Finland
SO PCT Int. Appl., 33 pp.
CODEN: PIXXD2

DT Patent
LA English
IC ICM C12P007-18
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): 10
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9301299	A1	19930121	WO 1992-FI203	19920630	<--
	W: CA, DE, FI, GB, JP, NL, NO					
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, MC, NL, SE					
	CA 2112374	AA	19930121	CA 1992-2112374	19920630	<--
	CA 2112374	C	20021029			
	EP 604429	A1	19940706	EP 1992-912764	19920630	<--
	EP 604429	B1	19991020			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, MC, NL, SE					
	JP 07500492	T2	19950119	JP 1993-501989	19920630	<--
	JP 3331343	B2	20021007			
	AT 185841	E	19991115	AT 1992-912764	19920630	<--
	ES 2140411	T3	20000301	ES 1992-912764	19920630	<--
	FR 2678637	A1	19930108	FR 1992-8109	19920701	<--
	FR 2678637	B1	19960209			
	US 6271007	B1	20010807	US 1994-194624	19940207	<--
PRAI	FI 1991-3197	A	19910701	<--		
	US 1992-905870	B1	19920630	<--		
	WO 1992-FI203	W	19920630	<--		

AB Xylitol is manufactured with **yeast** mutants defective in xylose metabolism Kluyveromyces marxianus was mutagenized with acriflavine or ethylmethane sulfonate the treated with benomyl. Strains unable to metabolize xylose effectively were selected on xylose- and nystatin-containing medium. Xylitol production rates of 2.8 g/L/h were achieved with one mutant.

ST xylitol manuf **yeast** mutant

IT Candida
Candida utilis
Hansenula
Kluyveromyces
Kluyveromyces marxianus
Kluyveromyces marxianus bulgaricus
Kluyveromyces marxianus lactis
Kluyveromyces marxianus marxianus
Pichia
(xylose metabolism mutants of, for xylitol manufacture)

IT Ribozymes
RL: BIOL (Biological study)
(**yeast** transformant containing, directed against xylose metabolism, xylitol manufacture with)

IT Ribonucleic acids
RL: BIOL (Biological study)
(antisense, **yeast** transformant containing, directed against xylose metabolism, xylitol manufacture with)

IT **9028-16-4, Xylitol dehydrogenase**
9030-58-4
RL: BIOL (Biological study)
(inactivating mutation in **gene** for, **yeast** for xylitol manufacture containing)

IT 87-99-0P, Xylitol
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manufacture of, **yeast** mutants for)

IT 58-86-6, Xylose, uses
RL: BIOL (Biological study)
(**yeast** deficient in metabolism of, in preparation of, xylitol manufacture in relation to)

L49 ANSWER 20 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1993:96990 HCAPLUS
DN 118:96990
ED Entered STN: 19 Mar 1993
TI Cloning and expression in Saccharomyces cerevisiae of the NAD(P)H-dependent **xylose reductase**-encoding **gene** (XYL1) from the xylose-assimilating **yeast** Pichia stipitis
AU Amore, Rene; Koetter, Peter; Kuester, Christina; Ciriacy, Michael; Hollenberg, Cornelis P.
CS Inst. Mikrobiol., Heinrich-Heine-Univ., Duesseldorf, 4000, Germany
SO Gene (**1991**), 109(1), 89-97
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
CC 7-5 (Enzymes)
Section cross-reference(s): **3**
AB The XYL1 **gene** of the **yeast** P. stipitis was isolated from a genomic library using a specific cDNA probe, and its nucleotide (nt) sequence was determined In the 5' noncoding region of the P. stipitis XYL1 **gene**, a TATAAA element (known to be necessary for transcription initiation in most **yeast genes**) is found at nt -81, and two CCAAT recognition motifs (often referred to as the CCAAT box) are present at nt -146 and -106. The XYL1 encodes a polypeptide of 35,927 Da that constitutes a NADH/NADPH-dependent **xylose reductase** (XR). The enzyme is part of the xylose-xylulose pathway that is absent or only weakly expressed in S. cerevisiae. Extensive homol. is found to the N terminus of the XR of Pachysolen tannophilus and Candida shehatae. None of the known cofactor binding domains found in many NAD-dependent dehydrogenases are present in the protein. Transformants of S. cerevisiae containing XYL1 of P. stipitis synthesize an active XR. Fusion of XYL1 with the prokaryotic tac promoter leads to a **gene** that can be expressed in S. cerevisiae and Escherichia coli.
ST **xylose reductase gene** Pichia sequence cloning
IT Pichia stipitis
(NADH/NADPH-dependent **xylose reductase gene** of, cloning and sequence and expression of)
IT Escherichia coli
Saccharomyces cerevisiae
(cloning in, of XYL1 **gene** of Pichia stipitis)
IT Deoxyribonucleic acid sequences
(for NADH/NADPH-dependent **xylose reductase gene**, of Pichia stipitis)
IT Protein sequences
(for NADH/NADPH-dependent **xylose reductase**, of Pichia stipitis)
IT Molecular cloning
(of XYL1 **gene** of Pichia stipitis, in Escherichia coli and Saccharomyces cerevisiae)
IT **Gene**, microbial
RL: BIOL (Biological study)
(XYL1, of Pichia stipitis, cloning and sequence and expression of)
IT **138263-97-5**, NADH/NADPH-dependent **xylose reductase** (Pichia stipitis λgt11 clone reduced)
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)
IT **95829-40-6**
RL: BIOL (Biological study)
(**gene** for, of Pichia stipitis, cloning and sequence and expression of)

IT 138575-99-2, **DNA** (Pichia stipitis λgt11 clone XYL1 **gene** and flanking region)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
IT 138575-98-1
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of, complete)

L49 ANSWER 21 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:52957 HCAPLUS
DN 116:52957
ED Entered STN: 21 Feb 1992
TI Cloning of **yeast xylose reductase** and **xylitol dehydrogenase genes** and their use
IN Strasser, Alexander W. M.; Hollenberg, Cornelis P.; Von Ciriacy-Wantrup, Michael; Koetter, Peter; Amore, Rene; Piontek, Michael; Hagedorn, Jutta
PA Rhein Biotech Gesellschaft fuer neue Biotechnologische Prozesse und Produkte m.b.H., Germany
SO Ger. Offen., 51 pp.
CODEN: GWXXBX
DT Patent
LA German
IC ICM C12N001-19
ICS C12N015-63; C12P019-34; C07H021-04; C07K015-04
CC 3-4 (Biochemical **Genetics**)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	DE 4009676	A1	19911002	DE 1990-4009676	19900326	<--
	DE 4009676	C2	19930909			
	EP 450430	A2	19911009	EP 1991-104558	19910322	<--
	EP 450430	A3	19920102			
	EP 450430	B1	19970625			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE					
	AT 154829	E	19970715	AT 1991-104558	19910322	<--
	ES 2104626	T3	19971016	ES 1991-104558	19910322	<--
	CA 2039021	AA	19910927	CA 1991-2039021	19910325	<--
	JP 06339383	A2	19941213	JP 1991-62160	19910326	<--
	JP 3122153	B2	20010109			
	JP 2000139486	A2	20000523	JP 2000-589	19910326	<--
	JP 2001103988	A2	20010417	JP 2000-276227	19910326	<--
	JP 3193917	B2	20010730			
PRAI	DE 1990-4009676	A	19900326	<--		
	JP 1991-62160	A3	19910326	<--		

AB The XYL1 **gene** encoding **xylose reductase** and the XYL2 **gene** encoding **xylitol dehydrogenase** of Pichia stipitis are cloned, sequenced, and expressed in other microorganisms. **Yeast** transformants expressing these **genes** can be used to prepare EtOH, alc. beverages, or biomass. The promoters of these **genes** can be used to express **genes** in **yeast.** A Saccharomyces cerevisiae mutant containing both **genes** was prepared and used to prepare EtOH in .apprx.80% yield from xylose. **Plasmids** containing Clostridium thermocellum cellulase **gene** linked to the promoter of XYL1 or XYL2 were prepared and P. stipitis transformed with them. These transformants produced the enzyme in response to xylose induction.
ST XYL1 XYL2 **gene** Pichia cloning; **xylose reductase gene** Pichia; **xylitol dehydrogenase gene** Pichia; Saccharomyces transformant ethanol manuf xylose
IT Fermentation
(alc., **yeast** expressing XYL1 and/or XYL2 **genes** of Pichia stipitis for)

IT Paecilomyces
Saccharomyces cerevisiae
Schizosaccharomyces
Schizosaccharomyces pombe
Zymomonas
(expression in, of XYL1 and XYL2 **genes** of Pichia stipitis)
IT Protein sequences
(of **xylitol dehydrogenase** of Pichia stipitis, complete)
IT Protein sequences
(of **xylose reductase** of Pichia stipitis, complete)
IT Molecular cloning
(of XYL1 and XYL2 **genes** of Pichia stipitis, in **yeast**)
IT **Plasmid** and Episome
(pMPGC1-2, cellulase **gene** of Clostridium on, expression in Pichia stipitis of)
IT **Plasmid** and Episome
(pR2, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pXDH, **xylitol dehydrogenase gene** XYL2 fragment of Pichia stipitis on)
IT **Plasmid** and Episome
(pXDH-HIS3, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)
IT **Plasmid** and Episome
(pXR, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pXR-LEU2, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)
IT **Plasmid** and Episome
(pXRa, **xylose reductase gene**, XYL1 fragment of Pichia stipitis on)
IT **Plasmid** and Episome
(pXRb, **xylose reductase gene** XYL1 fragment of Pichia stipitis on)
IT Biomass
(preparation of, **yeast** expressing XYL1 and/or XYL2 **genes** of Pichia stipitis for)
IT Deoxyribonucleic acid sequences
(**xylitol dehydrogenase**-specifying, of Pichia stipitis, complete)
IT Candida
Debaryomyces
Hansenula
Kluyveromyces
Metschnikowia
Pachysolen (fungus)
Pichia
Saccharomyces
Schwanniomyces
(**xylose reductase** and **xylitol dehydrogenase genes** of, cloning of, cloning of XYL1 and XYL2 **genes** of Pichia stipitis in relation to)
IT Deoxyribonucleic acid sequences
(**xylose reductase**-specifying, of Pichia stipitis, complete)
IT Pichia stipitis
(XYL1 and XYL2 **genes** of, cloning and expression in **yeast** of)
IT **Plasmid** and Episome

(pD1, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pD2, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pR1, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pRD1, **xylose reductase gene** XYL1 and **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT Genetic element
RL: BIOL (Biological study)
(promoter, of XYL1 and XYL2 **genes** of Pichia stipitis, heterologous **gene** expression in **yeast** using)
IT **Gene**, microbial
RL: BIOL (Biological study)
(XYL1, cloning and expression of, of Pichia stipitis, in **yeast**)
IT **Gene**, microbial
RL: BIOL (Biological study)
(XYL2, cloning and expression of, of Pichia stipitis, in **yeast**)
IT 136511-83-6 **138263-97-5**
RL: BIOL (Biological study)
(amino acid sequence of and expression in Saccharomyces of **gene** for)
IT 136510-54-8, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2) 136510-55-9, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2 plus 5'- and 3'-flanking region fragment) 138575-98-1, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1) 138575-99-2, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1 plus 5'- and 3'-flanking region fragment)
RL: BIOL (Biological study)
(cloning and expression in Saccharomyces and nucleotide sequence of)
IT 138575-97-0, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2 promoter region-containing fragment) 138576-00-8, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1 promoter region-containing fragment)
RL: PRP (Properties)
(**gene** expression in **yeast** using and nucleotide sequence of)
IT **9028-16-4, Xylitol dehydrogenase**
95829-40-6, Xylose reductase
RL: BIOL (Biological study)
(**gene** for, of Pichia stipitis, cloning and expression in **yeast** of)
IT 64-17-5P, Ethanol, preparation
RL: PREP (Preparation)
(manufacture of, **yeast** transformants expressing XYL1 and XYL2 **genes** of Pichia stipitis for)
IT 53-57-6P, NADPH 53-59-8P, NADP+
RL: PREP (Preparation)
(preparation of, from NADPH, **xylose reductase** of Pichia stipitis for)
IT 551-84-8, Xylulose
RL: BIOL (Biological study)
(**yeast** mutants growing on, XYL1 and XYL2 **genes** of Pichia stipitis expression in and enzyme manufacture with)
IT 58-86-6, Xylose, biological studies
RL: BIOL (Biological study)
(**yeast** transformed with XYL1 and/or XYL2 **genes** of

Pichia growth on, for biomass preparation)

L49 ANSWER 22 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1992:35663 HCAPLUS
DN 116:35663
ED Entered STN: 08 Feb 1992
TI Recombinant **yeasts** containing **DNA** sequences coding for **xylose reductase** and **xylitol dehydrogenase**
IN Hallborn, Johan; Penttila, Merja; Ojamo, Heikki; Walfridsson, Mats; Airaksinen, Ulla; Keranen, Sirkka; Hahn-Hagerdal, Barbel
PA Valtion Teknillinen Tutkimuskeskus, Finland
SO PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-53
ICS C12N009-04
CC 3-4 (Biochemical **Genetics**)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9115588	A1	19911017	WO 1991-FI103	19910408	<--
	W: AU, CA, FI, JP, NO, US					
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE					
	FI 9001771	A	19911007	FI 1990-1771	19900406	<--
	CA 2090122	AA	19911007	CA 1991-2090122	19910408	<--
	CA 2090122	C	20020618			
	AU 9175657	A1	19911030	AU 1991-75657	19910408	<--
	AU 647104	B2	19940317			
	EP 527758	A1	19930224	EP 1991-906996	19910408	<--
	EP 527758	B1	19980107			
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE					
	JP 05507843	T2	19931111	JP 1991-506907	19910408	<--
	JP 3348215	B2	20021120			
	AT 161886	E	19980115	AT 1991-906996	19910408	<--
	ES 2113373	T3	19980501	ES 1991-906996	19910408	<--
	NO 9203880	A	19921006	NO 1992-3880	19921006	<--
	US 5866382	A	19990202	US 1994-336198	19941103	<--
	US 6582944	B1	20030624	US 1999-184965	19990108	<--
	FI 9902153	A	19991006	FI 1999-2153	19991006	<--

PRAI	FI 1990-1771	A	19900406	<--
	US 1990-527775	A2	19900524	<--
	WO 1991-FI103	A	19910408	<--
	US 1992-848694	B1	19920309	<--
	FI 1992-4461	A	19921002	<--
	US 1994-336198	A3	19941103	<--

AB A cDNA for **yeast xylose reductase** is cloned and sequenced. This cDNA is expressed in recombinant **yeast**, optionally along with that for **xylitol dehydrogenase.** These recombinant **yeast** can be used to prepare xylitol, or ethanol (when both **genes** are expressed), from xylose or xylose-containing materials. The **xylose reductase** cDNA of Pichia stipitis was cloned. Saccharomyces cerevisiae transformants expressing this cDNA were used to prepare xylitol. S. cerevisiae expressing both **xylose reductase** and **xylitol dehydrogenase** produced EtOH, xylitol, and biomass from spent sulfite liquor.
ST **xylose reductase** cDNA Pichia cloning; xylitol ethanol manuf recombinant Saccharomyces
IT **Gene**, microbial
RL: BIOL (Biological study)
(cDNA, for **xylose reductase** of Pichia stipitis,

cloning and expression in Saccharomyces cerevisiae of)
IT Kluyveromyces
Pichia
Saccharomyces cerevisiae
Schizosaccharomyces pombe
Yeast
(expression in, of **xylose reductase** cDNA of Pichia stipitis)
IT Molecular cloning
(of **xylose reductase** cDNA of Pichia stipitis, in Saccharomyces cerevisiae)
IT Protein sequences
(of **xylose reductase** of Pichia stipitis, complete)
IT **Plasmid** and Episome
(pJHXDH60, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pJHXDH70, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pJHXR22, **xylose reductase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pMW22, **xylitol dehydrogenase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pUA103, **xylose reductase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT **Plasmid** and Episome
(pUA107, **xylose reductase** cDNA of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
IT Pichia stipitis
(**xylose reductase** cDNA of, cloning and expression in Saccharomyces cerevisiae of)
IT Deoxyribonucleic acid sequences
(**xylose reductase**-specifying, of Pichia stipitis, complete)
IT **138263-97-5**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of and cloning of cDNA for)
IT **95829-40-6, Xylose reductase**
RL: BIOL (Biological study)
(cDNA for, of Pichia stipitis, cloning and expression in Saccharomyces cerevisiae of)
IT **9028-16-4, Xylitol dehydrogenase**
RL: BIOL (Biological study)
(cDNA for, recombinant **yeast** expressing **xylose reductase** cDNA and, ethanol manufacture with)
IT 138263-60-2, Deoxyribonucleic acid (Pichia stipitis clone pUA103 **gene** xrd minus terminator fragment)
RL: PRP (Properties); BIOL (Biological study)
(cloning and nucleotide sequence of)
IT 87-99-0P, Xylitol
RL: PREP (Preparation)
(manufacture of, from xylose, recombinant **yeast xylose reductase** for)
IT 64-17-5P, Ethanol, preparation
RL: PREP (Preparation)
(manufacture of, recombinant **yeast** expressing **xylose reductase** and **xylitol dehydrogenase** cDNAs for)
IT 58-86-6, Xylose, biological studies
RL: BIOL (Biological study)

(xylitol manufacture from, recombinant **yeast** expressing cloned **xylose reductase** cDNA for)

L49 ANSWER 23 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1991:576285 HCAPLUS
DN 115:176285
ED Entered STN: 01 Nov 1991
TI Isolation and characterization of the Pichia stipitis **xylitol dehydrogenase gene**, XYL2, and construction of a xylose-utilizing Saccharomyces cerevisiae transformant
AU Koetter, Peter; Amore, Rene; Hollenberg, Cornelis P.; Ciriacy, Michael
CS Inst. Mikrobiol., Heinrich-Heine-Univ., Duesseldorf, W-4000, Germany
SO Current Genetics (**1990**), 18(6), 493-500
CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
CC 3-3 (Biochemical **Genetics**)
AB A P. stipitis cDNA library in λgt11 was screened using antisera against P. stipitis **xylose reductase** and **xylitol dehydrogenase**, resp. The resulting cDNA clones served as probes for screening a P. stipitis genomic library. The genomic XYL2 **gene** was isolated and the nucleotide sequence of the 1089-bp structural **gene**, and of adjacent non-coding regions, was determined The XYL2 open-reading frame codes for a protein of 363 amino acids with a predicted mol. mass of 38.5 kDA. The XYL2 **gene** is actively expressed in S. cerevisiae transformants. S. cerevisiae cells transformed with a **plasmid**, pRD1, containing both the **xylose reductase gene** (XYL1) and the **xylitol dehydrogenase gene** (XYL2), were able to grow on xylose as a sole carbon source. In contrast to aerobic glucose metabolism, S. cerevisiae XYL1-XYL2 transformants utilize xylose almost entirely oxidatively.
ST Pichia **xylitol dehydrogenase gene** XYL2 sequence; transformation Saccharomyces **xylitol dehydrogenase gene** Pichia
IT **Saccharomyces cerevisiae**
(cloning and expression in, of **xylitol dehydrogenase** and **xylose reductase genes** of Pichia stipitis)
IT Protein sequences
(of **xylitol dehydrogenase**, of Pichia stipitis, complete)
IT Transformation, genetic
(of Saccharomyces cerevisiae, with Pichia stipitis xylose metabolism **genes** XYL1 and XYL2)
IT Codon
RL: BIOL (Biological study)
(usage of, in **xylitol dehydrogenase gene** XYL2, of Pichia stipitis)
IT Pichia stipitis
(**xylitol dehydrogenase gene** XYL2 of, structure and cloning and expression in Saccharomyces cerevisiae of)
IT Deoxyribonucleic acid sequences
(**xylitol dehydrogenase**-specifying, of Pichia stipitis, complete)
IT **Plasmid** and Episome
(pRD1, cloning vector for **xylitol dehydrogenase** and **xylose reductase genes**, expression in Saccharomyces cerevisiae of)
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(XYL1, for **xylose reductase**, of Pichia stipitis, cloning and expression in Saccharomyces cerevisiae of)

IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(XYL2, for **xylitol dehydrogenase**, of Pichia stipitis, structure and cloning and expression in Saccharomyces cerevisiae of)
IT 136511-83-6
RL: PRP (Properties)
(amino acid sequence of)
IT **95829-40-6**, **Xylose reductase**
RL: PRP (Properties)
(**gene** for, of Pichia stipitis, cloning and expression in Saccharomyces cerevisiae of)
IT **9028-16-4**, **Xylitol dehydrogenase**
RL: PRP (Properties)
(**gene** for, of Pichia stipitis, sequence and expression in Saccharomyces cerevisiae of)
IT 58-86-6, Xylose, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by Saccharomyces cerevisiae transformant containing Pichia stipitis **genes** XYL1 and XYL2)
IT 136510-55-9, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2 plus 5'- and 3'-flanking region fragment)
RL: PRP (Properties)
(nucleotide sequence in)
IT 136510-54-8, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)

L49 ANSWER 24 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:492753 HCAPLUS
DN 113:92753
ED Entered STN: 16 Sep 1990
TI Isolation of cDNA clones using **yeast** artificial **chromosome** probes
AU Elvin, P.; Slynn, G.; Black, D.; Graham, A.; Butler, R.; Riley, J.; Anand, R.; Markham, A. F.
CS Eep. Biotechnol., ICI Pharm., Cheshire, SK10 4TG, UK
SO Nucleic Acids Research (**1990**), 18(13), 3913-17
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
CC 3-4 (Biochemical **Genetics**)
AB The cloning of large **DNA** fragments of hundreds of kilobases in **yeast** artificial **chromosomes** has simplified the anal. of regions of the genome previously cloned by cosmid walking. The mapping of expressed sequences within cosmid contigs has relied on the association of **genes** with sequence motifs defined by rare-cutting endonucleases, and the identification of sequence conservation between species. It was reasoned that if the contribution of repetitive sequences to filter hybridizations could be minimized, then the use of large cloned **DNAs** as hybridization probes to screen cDNA libraries would greatly simplify the characterization of hitherto unidentified **genes.** The use of this approach is demonstrated by using a YAC, containing 180kb of human genomic **DNA** including the **aldose reductase gene**, as a probe to isolate an **aldose reductase** cDNA from a λgt11 human fetal liver cDNA library.
ST human **aldose reductase** cDNA detection YAC; cDNA detection cosmid YAC **gene** probe; **yeast** artificial **chromosome** probe cDNA identification
IT **Gene** and Genetic element, animal
RL: BIOL (Biological study)

(for **aldose reductase**, of human, **yeast** artificial **chromosome** vector for isolation of cDNA for)
IT **Gene** and Genetic element
RL: BIOL (Biological study)
(isolation of, **yeast** artificial **chromosome** containing genomic inserts as probes for)
IT Molecular cloning
(**yeast** artificial **chromosome** as probe for, cDNA library screening with)
IT **Chromosome**
(**yeast** artificial, isolation of cDNA clones using **chromosomal** probes cloned in)
IT **9028-31-3**
RL: PRP (Properties)
(cDNA library containing sequence for human, homologous **gene** in **yeast** artificial **chromosome** as probe for detection of)

L49 ANSWER 25 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:422145 HCAPLUS
DN 113:22145
ED Entered STN: 21 Jul 1990
TI **Xylulokinase** activity in various **yeasts** including Saccharomyces cerevisiae containing the cloned **xylulokinase gene**
AU Deng, Xue Xing; **Ho, Nancy W. Y.**
CS A. A. Potter Eng. Cent., Purdue Univ., West Lafayette, IN, 47907, USA
SO Applied Biochemistry and Biotechnology (**1990**), 24-25, 193-9
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 16-5 (Fermentation and Bioindustrial Chemistry)
Section cross-reference(s): **3**, 10
AB D-Xylose is a major constituent of hemicellulose, which makes up 20-30% of the renewable biomass in nature. D-Xylose can be fermented by most **yeasts**, including S. cerevisiae, by a 2-stage process. In this process, xylose is 1st converted to xylulose in vitro by xylose (glucose) isomerase, and the latter sugar is then fermented by **yeast** to EtOH. With the availability of an inexpensive source of xylose isomerase produced by recombinant Escherichia coli, this process of fermenting xylose to EtOH can become quite effective. **Yeast** xylose and xylulose fermentation was further improved by cloning and overexpression of the **xylulokinase gene.** For instance, the level of **xylulokinase** activity in S. cerevisiae was increased 230-fold by cloning its **xylulokinase gene** on a high copy-number **plasmid**, coupled with fusion of the **gene** with an effective promoter. The resulting genetically engineered **yeasts** can ferment xylose and xylulose more than twice as fast as the parent **yeast.**
ST **xylulokinase gene** cloning **yeast** ethanol fermn; Saccharomyces xylulose fermn **xylulokinase gene**
IT Fermentation
(ethanol, from xylose by **yeast**, **xylulokinase gene** cloning in)
IT **Gene** and Genetic element, microbial
RL: PROC (Process)
(for **xylulokinase**, cloning of, in **yeast** for ethanol fermentation)
IT Molecular cloning
(of **xylulokinase gene**, in **yeast** for ethanol fermentation)
IT **Yeast**
(**xylulokinase** activities in)

IT **Saccharomyces cerevisiae**
(**xylulokinase gene** cloning in, for ethanol fermentation)
IT 58-86-6, Xylose, biological studies
RL: BIOL (Biological study)
(ethanol fermentation of, by **yeast**, **xylulokinase gene** cloning in)
IT **9030-58-4**, **Xylulokinase**
RL: BIOL (Biological study)
(**gene** for, cloning of, in **yeast** for ethanol fermentation)
IT 64-17-5P, Ethanol, preparation
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)
(manufacture of, from xylose by **yeast**, **xylulokinase gene** cloning in)

L49 ANSWER 26 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1990:94337 HCAPLUS
DN 112:94337
ED Entered STN: 18 Mar 1990
TI Purification, characterization, and amino terminal sequence of **xylose reductase** from Candida shehatae
AU **Ho, N. W. Y.**; Lin, F. P.; Huang, S.; Andrews, P. C.; Tsao, G. T.
CS Lab. Renewable Resourc. Eng., Purdue Univ., West Lafayette, IN, 47907, USA
SO Enzyme and Microbial Technology (**1990**), 12(1), 33-9
CODEN: EMTED2; ISSN: 0141-0229
DT Journal
LA English
CC 7-2 (Enzymes)
Section cross-reference(s): 16
AB A convenient and reliable procedure for the purification of **xylose reductase** from C. shehatae to near homogeneity was developed. The amino acid composition and N-terminal sequence of the enzyme were also analyzed. C. shehatae seems to contain only 1 **xylose reductase**, but the enzyme has a dual coenzyme specificity for both NADPH and NADH. The enzyme is remarkably stable at room temperature and 4°. Xylose fermentation is by NADH-dependent activity.
ST **xylose reductase** Candida; xylose fermn **xylose reductase** NADH Candida
IT Protein sequences
(of **xylose reductase** N-terminus, of Candida shehatae)
IT Amino acids, biological studies
RL: BIOL (Biological study)
(of **xylose reductase**, of Candida shehatae)
IT Fermentation
(of xylose, by **xylose reductase** of **yeast**, NADH-dependent activity in)
IT Candida shehatae
(**xylose reductase** of, purification and N-terminal amino acid sequence and other properties of)
IT 58-86-6, D-Xylose, biological studies
RL: BIOL (Biological study)
(fermentation of, by **yeast xylose reductase**, NADH-dependent activity in)
IT **95829-40-6P**, **Xylose reductase**
RL: PREP (Preparation)
(of Candida shehatae, purification and N-terminal amino acid sequence and other properties of)
IT 53-57-6, NADPH
RL: BIOL (Biological study)
(**xylose reductase** of Candida shehatae requirement for NADH and)
IT 58-68-4, NADH

RL: BIOL (Biological study)
(**xylose reductase** of Candida shehatae requirement for NADPH and)

L49 ANSWER 27 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:611729 HCAPLUS
DN 111:211729
ED Entered STN: 09 Dec 1989
TI Metabolism of D-xylose in Schizosaccharomyces pombe cloned with a xylose isomerase **gene**
AU Chan, Err Cheng; Ueng, Peter Pear; Chen, Li Fu
CS Dep. Food Sci., Purdue Univ., West Lafayette, IN, 47907, USA
SO Applied Microbiology and Biotechnology (**1989**), 31(5-6), 524-8
CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
CC 10-2 (Microbial Biochemistry)
Section cross-reference(s): **3**
AB The Escherichia coli xylose isomerase **gene** was transformed into S. pombe for direct D-xylose utilization. In order to understand D-xylose metabolism and determine the limiting factors on D-xylose utilization by the transformed **yeast**, D-xylose transport, xylose isomerization, and xylulose phosphorylation were investigated. The results indicated that low activity of xylose isomerization in the cloned **yeast** was the limiting step for D-xylose fermentation An in vitro study showed that **yeast** proteases decreased xylose isomerase activity. Xylitol, a byproduct of D-xylose fermentation, had no effect on the activity of xylose isomerase.
ST xylose metab Schizosaccharomyces **gene** cloning; Escherichia xylose isomerase **gene** cloning **yeast**
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(for xylose isomerase, of Escherichia coli, xylose metabolism by recombinant Schizosaccharomyces pombe containing)
IT Biological transport
(of xylose, by recombinant xylose isomerase-containing Schizosaccharomyces pombe)
IT Schizosaccharomyces pombe
(xylose metabolism by recombinant xylose isomerase-containing)
IT 58-86-6, D-Xylose, biological studies 551-84-8, D-Xylulose
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metabolism of, by Schizosaccharomyces pombe with xylose isomerase **gene**)
IT **9030-58-4**, **Xylulokinase**
RL: BIOL (Biological study)
(of transformed Schizosaccharomyces pombe containing xylose isomerase)
IT 9023-82-9, Xylose isomerase
RL: BIOL (Biological study)
(of Escherichia coli, xylose metabolism by Schizosaccharomyces pombe with)

L49 ANSWER 28 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:510301 HCAPLUS
DN 111:110301
ED Entered STN: 01 Oct 1989
TI Construction of **yeast xylulokinase** mutant by recombinant **DNA** techniques
AU Stevis, Panayiotis E.; **Ho, Nancy W. Y.**
CS Dep. Foods Nutr., Purdue Univ., West Lafayette, IN, 47907, USA
SO Applied Biochemistry and Biotechnology (**1989**), Volume Date 1988, 20-21, 327-34
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal

LA English
CC 3-5 (Biochemical **Genetics**)
AB A Saccharomyces cerevisiae **xylulokinase** mutant was constructed by using the cloned **yeast xylulokinase gene**, XYK-Sc, and the **gene** disruption technique. The S. cerevisiae LEU2 **gene** was used to disrupt the XYK-Sc **gene** cloned on pLSK4 by insertion into the unique HindIII site of the **gene.** The disrupted **gene** was liberated from the remainder of the **plasmid** with XhoI digestion, yielding a 4.4 kb **DNA** fragment. Transformation of a S. cerevisiae leu2 mutant with this fragment and selection for Leu+ complementation resulted in the isolation of transformants that were unable to grow in pure xylulose medium. The ability to grow in xylulose medium and increased **xylulokinase** activity were obtained by transforming the mutant with a **plasmid** -borne wild-type XYK-Sc **gene.** Insertional inactivation of the **chromosomal** XYK-Sc **gene** was also demonstrated by xululokinase assays.
ST Saccharomyces **xylulokinase gene** mutation recombinant **DNA**
IT Mutation
(in **xylulokinase gene**, of Saccharomyces cerevisiae, **gene** disruption technique in construction of)
IT **Saccharomyces cerevisiae**
(**xylulokinase gene** of, mutation construction in, by **gene** disruption technique)
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(XYK, for **xylulokinase**, of Saccharomyces cerevisiae, mutation in, **gene** disruption technique for)
IT **9030-58-4**, **Xylulokinase**
RL: PRP (Properties)
(**gene** for, of Saccharomyces cerevisiae, construction of mutation in, by **gene** disruption technique)

L49 ANSWER 29 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:472444 HCAPLUS
DN 111:72444
ED Entered STN: 03 Sep 1989
TI Cloning of **yeast xylulokinase gene** by complementation of E. coli and **yeast** mutations
AU **Ho, Nancy W. Y.**; Chang, Sue Fen
CS Lab. Renew. Resour. Eng., Purdue Univ., West Lafayette, IN, USA
SO Enzyme and Microbial Technology (**1989**), 11(7), 417-21
CODEN: EMTED2; ISSN: 0141-0229
DT Journal
LA English
CC 3-4 (Biochemical **Genetics**)
AB The **gene** encoding **yeast** (Saccharomyces cerevisiae) **xylulokinase** has been isolated by complementation of Escherichia coli **xylulokinase** mutations. Through subcloning, the **gene** has been localized on two HindIII fragments (1.2 and 2.4 bp). Within these HindIII fragments, there lies a 2.2-kb Xho fragment which contains the structural **gene** of **yeast xylulokinase.** Upon insertion of a selectable **gene** into the XhoI fragment, the resulting recombination fragment has been used to construct a **yeast xylulokinase** mutant by the **gene** disruption technique. The cloned **xylulokinase gene** was found to be able to complement such a **xylulokinase** mutant.
ST Saccharomyces **xylulokinase gene** cloning Escherichia
IT **Gene** and Genetic element, microbial
RL: PROC (Process)
(for **xylulokinase**, of **yeast**, cloning of)

IT Complementation, genetic
(of **xylulokinase gene** mutation in Escherichia coli, by **yeast gene**)
IT Molecular cloning
(of **xylulokinase gene**, of **yeast**)
IT **Saccharomyces cerevisiae**
(**xylulokinase gene** of, cloning of)
IT Escherichia coli
(**xylulokinase gene** of, mutation in, **yeast gene** complementation of)
IT **9030-58-4**, **Xylulokinase**
RL: PRP (Properties)
(**gene** for, of **yeast**, cloning of)

L49 ANSWER 30 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:434409 HCAPLUS
DN 111:34409
ED Entered STN: 05 Aug 1989
TI A nuclear **yeast gene** (GCY) encodes a polypeptide with high homology to a vertebrate eye lens protein
AU Oechsner, Ulrich; Magdolen, Viktor; Bandlow, Wolfhard
CS Inst. Genet. Microbiol., Munich, D-8000, Fed. Rep. Ger.
SO FEBS Letters (**1988**), 238(1), 123-8
CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
CC 3-3 (Biochemical **Genetics**)
Section cross-reference(s): 6
AB The nuclear **gene** for a **yeast** protein is described which shows unexpectedly high homol. with mammalian aldo/keto reductases as well as with ρ-crystallin, one of the prominent proteins of the frog eye lens. Although it could be proven that the **gene** occurs as a single copy in the haploid **yeast** genome, replacement of the intact by a disrupted, nonfunctional allele led to no obvious phenotype, indicating that the **gene** is dispensable. The **gene** was assigned to **chromosome** XV. It is transcribed in vivo into an mRNA of about 1300 bases with a coding capacity for a protein of 312 amino acids (estimated Mr, 35,000).
ST Saccharomyces **gene** GCY protein sequence
IT **Saccharomyces cerevisiae**
(**gene** GCY protein of, homol. of, to vertebrate eye lens protein)
IT Protein sequences
(of **gene** GCY protein, of Saccharomyces cerevisiae, complete)
IT Eye, composition
(protein of, of vertebrate, **gene** GCY protein of Saccharomyces cerevisiae homol. with)
IT Proteins, specific or class
RL: BIOL (Biological study)
(**gene** GCY, **gene** for, of Saccharomyces cerevisiae, nucleotide and encoded peptide sequences of)
IT Deoxyribonucleic acid sequences
(**gene** GCY protein-specifying, of Saccharomyces cerevisiae, complete)
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(GCY, of Saccharomyces cerevisiae, nucleotide and encoded peptide sequences of)
IT Crystallins
RL: BIOL (Biological study)
(ρ-, **gene** GCY protein of Saccharomyces cerevisiae homol. with, of frog)
IT **Chromosome**

(Saccharomyces cerevisiae XV, **gene** GCY localization on)
IT **121548-71-8**, Protein (Saccharomyces cerevisiae **gene** GCY reduced)
RL: PRP (Properties)
(amino acid sequence of)
IT 121547-66-8, Deoxyribonucleic acid (Saccharomyces cerevisiae **gene** GCY)
RL: PRP (Properties); BIOL (Biological study)
(nucleotide sequence of)
IT **9028-31-3**
RL: PRP (Properties)
(of eye lens, of rat, **gene** GCY protein of Saccharomyces cerevisiae homol. with)
IT 9028-12-0, Aldehyde reductase
RL: PRP (Properties)
(of liver of human, **gene** GCY protein of Saccharomyces cerevisiae homol. with)
IT 55976-95-9
RL: PRP (Properties)
(of lung of cattle, **gene** GCY protein of Saccharomyces cerevisiae homol. with)

L49 ANSWER 31 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:129846 HCAPLUS
DN 110:129846
ED Entered STN: 15 Apr 1989
TI Cloning the **yeast xylulokinase gene** for the improvement of xylose fermentation
AU Chang, Sue Feng; **Ho, Nancy W. Y.**
CS Lab. Renew. Resour. Eng., Purdue Univ., West Lafayettye, IN, 47907, USA
SO Applied Biochemistry and Biotechnology (**1988**), 17, 313-18
CODEN: ABIBDL; ISSN: 0273-2289
DT Journal
LA English
CC 3-4 (Biochemical **Genetics**)
Section cross-reference(s): 16
AB **Plasmids** pLSK1 or pLSK3 containing a Saccharomyces cerevisiae **DNA** fragment complemented Escherichia coli **xylulokinase** mutations. The cloned **yeast DNA** probably contains all the necessary structural elements of a **yeast gene** encoding a **yeast** protein (enzyme). E. coli **xylulokinase** mutants harboring either pLSK1 or pLSK3 synthesized **xylulokinase** in the absence of xylose induction as well as in the presence of glucose (insensitive to glucose inhibition). Thus, the **yeast DNA** fragment cloned on pLSK1 or pLSK3 at least contains the structural **gene** encoding S. cerevisiae **xylulokinase.**
ST **xylulokinase gene** Saccharomyces complementation Escherichia
IT Escherichia coli
(expression in, of **xylulokinase gene** of Saccharomyces cerevisiae)
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(for **xylulokinase**, of Saccharomyces cerevisiae, structure and expression in Escherichia coli of)
IT Complementation, genetic
(of **xylulokinase** mutants of Escherichia coli, by Saccharomyces cerevisiae **gene**)
IT **Saccharomyces cerevisiae**
(**xylulokinase gene** of, structure and expression in Escherichia coli of)
IT **9030-58-4, Xylulokinase**
RL: PRP (Properties)

(**gene** for, of **yeast**, structure and expression in Escherichia coli of)

L49 ANSWER 32 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1988:33023 HCAPLUS
DN 108:33023
ED Entered STN: 06 Feb 1988
TI Cloning of the Pachysolen tannophilus **xylulokinase gene** by complementation in Escherichia coli
AU Stevis, Panayiotis E.; Huang, James J.; **Ho, Nancy W. Y.**
CS Lab. Renewable Resour. Eng., Purdue Univ., West Lafayette, IN, 47907, USA
SO Applied and Environmental Microbiology (**1987**), 53(12), 2975-7
CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
CC 3-4 (Biochemical **Genetics**)
AB The **gene** coding for **xylulokinase** has been isolated from the **yeast** P. tannophilus by complementation of E. coli **xylulokinase** (xylB) mutants. Through subcloning, the **gene** has been localized at one end of a 3.2-kilobase EcoRI-PstI fragment. Expression of the cloned **gene** was insensitive to glucose inhibition. Further, the cloned **gene** did not cross-hybridize with E. coli and Saccharomyces cerevisiae **xylulokinase genes.**
ST Pachysolen **xylulokinase gene** cloning Escherichia
IT Escherichia coli
(cloning in, of **xylulokinase gene** of Pachysolen tannophilus)
IT Molecular cloning
(of **xylulokinase gene** of Pachysolen tannophilus, in Escherichia coli)
IT Pachysolen tannophilus
(**xylulokinase gene** of, cloning in Escherichia coli of)
IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(XYK, for **xylulokinase**, of Pachysolen tannophilus, cloning in Escherichia coli of)
IT **9030-58-4**, **Xylulokinase**
RL: PRP (Properties)
(**gene** for, of Pachysolen tannophilus, cloning in Escherichia coli of)

L49 ANSWER 33 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 1986:419795 HCAPLUS
DN 105:19795
ED Entered STN: 26 Jul 1986
TI Towards a xylose fermenting **yeast**
AU Hollenberg, Cornelis P.; Wilhelm, Martin
CS Inst. Mikrobiol., Univ. Duesseldorf, Duesseldorf, 4000, Fed. Rep. Ger.
SO Eur. Congr. Biotechnol., 3rd (**1984**), Volume 3, 175-9 Publisher: Verlag Chemie, Weinheim, Fed. Rep. Ger.
CODEN: 55BBA6
DT Conference
LA English
CC 3-4 (Biochemical **Genetics**)
AB As a 1st step towards the cloning and expression of the xylose isomerase [9023-82-9] **gene** of Bacillus subtilis in Saccharomyces cerevisiae, a **DNA** fragment for B. subtilis was isolated which encodes xylose isomerase and **xylulokinase** [**9030-58-4**]. The **DNA** fragment was cloned on recombinant **plasmids** and used to transform an Escherichia coli strain that was isomerase deficient. The **plasmids** pMW1 and pMW11 were largely identical

except for a region of .apprx.1 kilobase absent from pMW11. **Plasmid** pMW11 contained the originally cloned B. subtilis **DNA** fragment which had been changed in pMW1 by the addition of an insertion element. The presence of pMW1 in E. coli transformants led to wild-type levels of isomerase activity, whereas in pMW11 transformants almost no activity could be detected. Thus, the expression of the B. subtilis **gene** was observed only after the insertion of an IS element. Furthermore, the expression of the xylose isomerase from pMW1 was not subjected to regulation in the E. coli transformants. The transformants also expressed high levels of **xylulokinase.**

ST xylose isomerase **gene** Bacillus cloning; **yeast** xylose fermn cloning

IT Escherichia coli
(cloning in, of xylose isomerase and **xylulokinase genes** of Bacillus subtilis)

IT **Gene** and Genetic element, microbial
RL: BIOL (Biological study)
(for xylose isomerase and **xylulokinase**, of Bacillus subtilis, cloning and expression in Escherichia coli of)

IT Molecular cloning
(of xylose isomerase and **xylulokinase genes**, of Bacillus subtilis in Escherichia coli)

IT Bacillus subtilis
(xylose isomerase and **xylulokinase genes** of, cloning in Escherichia coli of)

IT **Gene** and Genetic element, microbial
(insertion sequence, xylose isomerase **gene** containing, of Bacillus subtilis, Escherichia coli expression of)

IT **Plasmid** and Episome
(pMW1, xylose isomerase and **xylulokinase genes** of Bacillus subtilis cloning on, for expression in Escherichia coli)

IT 9023-82-9 **9030-58-4**
RL: PRP (Properties)
(**gene** for, of Bacillus subtilis, cloning and expression in Escherichia coli of)

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L66 ANSWER 1 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2003-748653** [70] WPIX
DNC **C2003-205320**
TI Improvement of ethanol production from xylose employs strain of **Saccharomyces** cerevisiae additionally comprising specific **genes** that are over-expressed.
DC D16 E17 H06
IN HAHN-HAEGERDAL, B; JOENSSON, L; WAHLBOM, F
PA (FORS-N) FORSKARPATENT I SYD AB
CYC 102
PI WO 2003078642 A1 20030925 (200370)* EN 28p C12P007-10
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW
ADT WO 2003078642 A1 WO 2003-SE397 20030311
PRAI SE 2002-855 20020319
IC ICM C12P007-10
ICS C12N001-19
AB WO2003078642 A UPAB: 20031030
NOVELTY - Improving ethanol production from xylose employs strain of **Saccharomyces** cerevisiae additionally comprising over-expressed PET18 (YCR020c), HXT5 (YHR096c), GAL2 (YLR081w), SOL3 (YHR163w), GND1 (YHR183w), TAL1 (YLR354c), TKL1 (YPR074c), PCK1 (YKR097w), ICL1 (YER065c), MLS1 (YNL117w), GAL1 (YBR020c), GAL7 (YBR018c), GAL10 (YBR019c), and/or CAT8 (YMR280c) **genes.** Open reading frames are given in brackets.
DETAILED DESCRIPTION - Improving ethanol production from xylose employs strain of **Saccharomyces** cerevisiae comprising **genes** for over-expression of **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase** and additionally over-expressed PET18 (YCR020c), HXT5 (YHR096c), GAL2 (YLR081w), SOL3 (YHR163w), GND1 (YHR183w), TAL1 (YLR354c), TKL1 (YPR074c), PCK1 (YKR097w), ICL1 (YER065c), MLS1 (YNL117w), GAL1 (YBR020c), GAL7 (YBR018c), GAL10 (YBR019c), and/or CAT8 (YMR280c) **genes.** Open reading frames are given in brackets.
USE - For improving ethanol production from xylose.
ADVANTAGE - The invention improves xylose utilization.
Dwg.0/0
FS CPI
FA AB; DCN
MC CPI: D05-B03; E10-E04E2; E11-M; H06-B
TECH UPTX: 20031030
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: TEC1 (YBR083w), ARR1 (YPR199c), MIG1 (YGL035c), and/or MIG2 (YGL209w) are deleted. One or more of the **genes** is over expressed and one or more of the **genes** is deleted.

L66 ANSWER 2 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2002-097582** [13] WPIX
DNC **C2002-030382**
TI Obtaining recombinant **yeast** of **Saccharomyces** cerevisiae for fermenting lignocellulose raw materials to ethanol, comprises introducing **deoxyribonucleic** acid into **yeast**
.
DC D16 D17 E17
IN CORDERO OTERO, R R; HAHN-HAEGERDAL, B; VAN ZYL, W H; HAHN-HAGERDAL, B; HAHNAEGERDAL, B

PA (FORS-N) FORSKARPATENT I SYD; (FORS-N) FORSKARPATENT I SYD AB; (OTER-I) CORDERO OTERO R R; (HAHN-I) HAHN-HAGERDAL B; (VZYL-I) VAN ZYL W H

CYC 96

PI WO 2001088094 A1 20011122 (200213)* EN 18p C12N001-19
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001058985 A 20011126 (200222) C12N001-19
EP 1282686 A1 20030212 (200312) EN C12N001-19
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
US 2003157675 A1 20030821 (200356) C12P007-06
ZA 2002009448 A 20031231 (200408) 29p C12N000-00

ADT WO 2001088094 A1 WO 2001-SE1061 20010515; AU 2001058985 A AU 2001-58985 20010515; EP 1282686 A1 EP 2001-932462 20010515, WO 2001-SE1061 20010515; US 2003157675 A1 Cont of WO 2001-SE1061 20010515, US 2002-293255 20021114; ZA 2002009448 A ZA 2002-9448 20021120

FDT AU 2001058985 A Based on WO 2001088094; EP 1282686 A1 Based on WO 2001088094

PRAI ZA 2000-2363 20000515

IC ICM C12N000-00; C12N001-19; C12P007-06
ICS C12N001-18; C12N015-74; C12P007-10

AB WO 200188094 A UPAB: 20020226
NOVELTY - Obtaining recombinant **yeast** of **Saccharomyces** cerevisiae, comprising introducing **DNA** into a **yeast**, where the obtained **yeast** introduces **genes** encoding **xylose reductase**, xylithol dehydrogenase and **xylulokinase**, is new.
USE - For obtaining recombinant **yeast** of **Saccharomyces** cerevisiae useful for fermenting lignocellulose raw materials to produce ethanol.
ADVANTAGE - The obtained recombinant **yeast** is efficiently capable of fermenting lignocellulose raw materials to produce ethanol.
Dwg.0/2

FS CPI

FA AB; DCN

MC CPI: D05-B03; D05-C03B; **D05-H05**; **D05-H08**; **D05-H12A**; **D05-H17A3**; E10-E04E2

TECH UPTX: 20020226
TECHNOLOGY FOCUS - BIOLOGY - Preferred Product: The **yeast** is capable of producing one or more lignocellulose utilizing enzymes of **xylose reductase**, xylithol dehydrogenase, or **xylulokinase.** Preferred Enzymes: The enzymes of the **yeast** is of the genus **Saccharomyces** cerevisiae and Pichia stipitis. The **xylose reductase** or **xylitol dehydrogenase** lignocellulose utilizing enzyme can be obtained from Pichia stipitis. The **xylulokinase** enzyme is obtained from **Saccharomyces** cerevisiae. Preferred Medium: The growth medium by the recombinant **yeast** comprises glucose and xylose. Preferred Method: The method includes isolating mutants by ethyl methanesulfonate treatment. The mutants show a growth rate over basic strain of more than 30%. The recombinant strain is maintained in continuous culture on xylose as carbon source at dilution rate of 0.1/h with growth rate on xylose of 0.14-0.15/h and biomass yield of 0.4 g/g on xylose at aerobic growth. It utilizes 20 g/L and 15-16 g/L of xylose (4-5 g/L residual) in a continuous culture from a 20 g/L xylose and 20 g/L of glucose feed. Preferred Strain: The **Saccharomyces** cerevisiae strain is **Saccharomyces** cerevisiae USM21, which has been deposited under CBS 102678. It is (non-)detoxified lignocellulose hydrolysates, or (soft or hard)wood derived hydrolysate. Preferred Mutants: The mutant is a xylose-fermenting

mutant XYLUSM125, which is deposited under CBS 102679 or XYLUSM145, which is deposited under CBS 102680.

ABEX UPTX: 20020226

EXAMPLE - XYLUSM125 mutant was grown in 20 g/L xylose in minimal medium and established XYLUSM125 in a continuous culture on 20 g/L xylose using dilution rate of 0.1/h (aerobic fermentation condition). The growth rate obtained on xylose as carbon source was 0.14-0.15/h and the biomass yield was 0.4 g/g to have 8 g/L biomass on 20 g/L xylose as carbon source. When the feed was changed to 20 g/L xylose and 20 g/L glucose the biomass had raised to 18 g/L and the result was only 4-5 g/L xylose remained. The XYLUSM125 mutant utilized 20 g/L glucose and 15-16 g/L xylose in continuous fermentation.

L66 ANSWER 3 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2002-097498** [13] WPIX
DNC **C2002-030322**
TI Site-specific insertion in Zymomonas mobilis, comprises transforming Zymomonas through homologous recombination with **deoxyribonucleic** acid fragment having interrupted sequence.
DC D16 E17
IN CHOU, Y; ZHANG, M
PA (MIDE) MIDWEST RES INST
CYC 95
PI WO 2001083784 A2 20011108 (200213)* EN 27p C12N015-63
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
CA 2304927 A1 20011102 (200213) EN C12N001-21
AU 2001051397 A 20011112 (200222) C12N015-63
JP 2003531620 W 20031028 (200373) 33p C12N015-09
EP 1366178 A2 20031203 (200380) EN C12N015-90
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
BR 2001010676 A 20031230 (200409) C12N015-63
ADT WO 2001083784 A2 WO 2001-US11239 20010406; CA 2304927 A1 CA 2000-2304927 20000502; AU 2001051397 A AU 2001-51397 20010406; JP 2003531620 W JP 2001-580391 20010406, WO 2001-US11239 20010406; EP 1366178 A2 EP 2001-924773 20010406, WO 2001-US11239 20010406; BR 2001010676 A BR 2001-10676 20010406, WO 2001-US11239 20010406
FDT AU 2001051397 A Based on WO 2001083784; JP 2003531620 W Based on WO 2001083784; EP 1366178 A2 Based on WO 2001083784; BR 2001010676 A Based on WO 2001083784
PRAI CA 2000-2304927 20000502; US 2000-562613 20000501
IC ICM C12N001-21; C12N015-09; C12N015-63; C12N015-90
ICS C12N015-11
AB WO 200183784 A UPAB: 20020226
NOVELTY - Site-specific insertion in Zymomonas, comprising interrupting a sequence in a Zymomonas **deoxyribonucleic** acid (**DNA**) fragment and transforming the Zymomonas through homologous recombination with the interrupted fragment, is new.
USE - For insertion inactivation of specific **gene** products in recombinant Z. mobilis strains which ferment xylose and/or arabinose into ethanol.
ADVANTAGE - The method eliminates the formation of by-products in a Z. mobilis fermentation through the construction of stable recombinant strains to be eliminated.
Dwg.0/10
FS CPI
FA AB; DCN
MC CPI: D05-B03; **D05-H05**; **D05-H09**; **D05-H12A**;

D05-H17A6; E10-E04E2

TECH UPTX: 20020226

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: Interrupting is by inserting a **DNA** sequence inside the **DNA** fragment or by deleting a **DNA** sequence inside the **DNA** fragment. The **DNA** fragment (e.g., ldh) is encoding a structural protein in a metabolic pathway of the by-product (e.g., lactic acid) to be eliminated. The interrupted **DNA** fragment is ligated with a **plasmid** vector. Transforming the Zymomonas mobilis organism is through homologous recombination with the interrupted fragment of the **plasmid** vector. The Z. mobilis of the **plasmid** is cured.

TECHNOLOGY FOCUS - BIOLOGY - Preferred **Plasmid**: The **plasmid** is pZB101, pZB102 or pZB121. It may be pZB1962-ldhL-ara. Preferred Insertion: The insertion is ldhL, a selection marker or an operon. The operon encodes structural **gene**(s) including xylose isomerase, **xylulokinase**, L-arabinose isomerase, L-ribulokinase, L-ribulose-5-phosphate-4-epimerase, transaldolase or transketolase, and a promoter for expression of the structural **gene** in Z. mobilis.

ABEX UPTX: 20020226

EXAMPLE - **Plasmids** containing ldh **gene** of Zymomonas having a tetracycline (Tc) resistant **gene** insert (1dh::Tc) cassette were used to transform Z. mobilis. The resultant Tc resistance transformants were analyzed by Southern hybridization. Results showed that the ldh::Tc cassette had been inserted into the ldh region of the Zymomonas genome. The **gene** integration based on homologous recombination in Zymomonas, together with the targeted integration resulting in an inactivated ldh **gene**, eliminated lactic acid by-product formation in ethanol fermentation.

L66 ANSWER 4 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2002-089743** [12] WPIX
CR 2003-731102 [69]
DNC **C2002-027635**
TI Transposon for **plasmid** vector for constructing strains of Zymomonas mobilis for conversion of pentose sugars into ethanol, comprises operon(s) having structural **genes** encoding enzymes and promoter(s).
DC D16 E17 H06
IN CHOU, Y; ZHANG, M
PA (MIDE) MIDWEST RES INST; (CHOU-I) CHOU Y; (ZHAN-I) ZHANG M
CYC 96
PI WO 2001083786 A2 20011108 (200212)* EN 49p C12N015-74
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
CA 2304929 A1 20011102 (200212) EN C12N001-21
AU 2001049926 A 20011112 (200222) C12N015-74
US 2002151034 A1 20021017 (200270) C12N001-20
EP 1278876 A2 20030129 (200310) EN C12N015-74
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
ADT WO 2001083786 A2 WO 2001-US11334 20010406; CA 2304929 A1 CA 2000-2304929 20000502; AU 2001049926 A AU 2001-49926 20010406; US 2002151034 A1 US 2000-565233 20000501; EP 1278876 A2 EP 2001-923213 20010406, WO 2001-US11334 20010406
FDT AU 2001049926 A Based on WO 2001083786; EP 1278876 A2 Based on WO 2001083786
PRAI CA 2000-2304929 20000502; US 2000-565233 20000501
IC ICM C12N001-20; C12N001-21; C12N015-74

ICS C12N015-09; C12N015-11; C12N015-52; C12N015-63; C12N015-90; C12P007-04; C12P007-06

AB WO 200183786 A UPAB: 20031027
NOVELTY - A transposon for stable insertion of foreign **genes** into a bacterial genome, comprising operon(s) having xylAxylB, araBAD or tal/tkt as structural **genes** encoding enzymes, and promoter(s) for expression of the structural **genes** in the bacterium, where the operons are contained inside a pair of inverted insertion sequences, and a transposase **gene** is located outside of the insertion sequences, is new.
USE - The transposon, e.g., Tn5 or Tn10 derivative, is for a **plasmid** vector (e.g., pZB1862-1dhL-ara ATCC Accession Number PTA-1798) which transforms a bacterium, i.e. Zymomonas mobilis (claimed). The strains of Z. mobilis (e.g., G8 ATCC Accession Number PTA-1796, C25 ATCC Accession Number PTA-1799, and AX ATCC Accession Number PTA-1797) are useful in the conversion of the cellulose derived pentose sugars, e.g., xylose and arabinose, into fuels and chemicals, e.g. ethanol.
ADVANTAGE - The invention provides for the construction of Z. mobilis strains which are capable of fermenting xylose and/or arabinose to ethanol through the generation of stable genomic inserts which encode the enzymes necessary for xylose and arabinose catabolism. The strains are free of antibiotic resistance and stable for more than 40 (at least 45) generations in a non-selection media. The strains also demonstrate a high specific rate of product formation at close to maximum theoretical product yield.
Dwg.0/18

FS CPI
FA AB; DCN
MC CPI: D05-B03; D05-C07; **D05-H12D5**; **D05-H12E**; E10-E04L2; H06-B
TECH UPTX: 20020221
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Component: The promoter is Peno or Pgap.
ABEX UPTX: 20020221
EXAMPLE - Two operons containing Pgap-xylA/xylB and Peno-talB/tktA were assembled in mini-Tn5 and the resulting **plasmid** was conjugated into Z. mobilis. With the help of the transposase located outside of the mini-Tn5 cassette, single copies of the two operons were inserted into the Z. mobilis genome. Enzymatic analysis of xylose isomerase, **xylulokinase**, transaldolase, and transketolase indicated that all the **genes** coordinately expressed and that the integrated strains produced 30-70% of the enzymatic activities of the **plasmid** -bearing strains. These enzymatic levels were enough for the organism to grow and ferment xylose to ethanol.

L66 ANSWER 5 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **2000-526176** [48] WPIX
DNC **C2000-156444**
TI **Genetically** modified microorganism useful for producing xylitol from D-xylulose comprises an exogenous **xylitol dehydrogenase gene.**
DC B05 D13 D16 D17 E17
IN TAKENAKA, Y; TONOUCHI, N; YOKOZEKI, K
PA (AJIN) AJINOMOTO KK; (AJIN) AJINOMOTO CO INC
CYC 30
PI EP 1029925 A1 20000823 (200048)* EN 21p C12P007-18
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI
JP 2000295994 A 20001024 (200059) 16p C12N015-09
CN 1271017 A 20001025 (200104) C12P007-18
KR 2000076625 A 20001226 (200134) C12N001-00
BR 2000000338 A 20010821 (200155) C12P007-18
US 2003148482 A1 20030807 (200358) C12P007-18

ADT EP 1029925 A1 EP 2000-102566 20000207; JP 2000295994 A JP 1999-197621 19990712; CN 1271017 A CN 2000-105396 20000209; KR 2000076625 A KR 2000-5838 20000208; BR 2000000338 A BR 2000-338 20000208; US 2003148482 A1 Cont of US 2000-500908 20000209, US 2002-277706 20021023
PRAI JP 1999-197621 19990712; JP 1999-31464 19990209
IC ICM C12N001-00; C12N015-09; C12P007-18
ICS C12N001-20; C12N009-04; C12N015-00; C12N015-74
ICA C12N001-21
AB EP 1029925 A UPAB: 20001001
NOVELTY - Microorganism (I) that has been transformed with a **gene** encoding **xylitol dehydrogenase** (XDH) and is capable of supplying reducing power to its culture medium (i.e. of producing sufficient reduced nicotinamide adenine **dinucleotide** (NADH) for XDH-catalyzed conversion of D-xylulose to xylitol) is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a process for producing xylitol by reacting a microorganism of type (I) with D-xylulose and collecting the resulting xylitol.

USE - The xylitol is useful as a low-calorie, non-carcinogenic sweetener and for fluid therapy in the treatment of diabetes.

ADVANTAGE - (I) is capable of converting D-xylulose to xylitol in the absence of added carbon sources or NADH.

Dwg.0/0
FS CPI
FA AB; DCN
MC CPI: B04-F10A3E; B10-A07; B14-S04; D03-H01A; D05-C03B; D05-C08; **D05-H12A**; **D05-H14A1**; **D05-H17A3**; D06-G; E10-A07
TECH UPTX: 20001001
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Process: The D-xylulose is produced by means of a microorganism (II) capable of converting D-arabitol to D-xylulose or a microorganism (III) capable of producing D-xylulose from glucose. Preferred Microorganisms: (I) is an Escherichia coli transformant. (II) is a microorganism of the genus Gluconobacter, Achromobacter, Agrobacterium, Alcaligenes, Arthrobacter, Azotobacter, Brevibacterium, Corynebacterium, Enterobacter, Erwinia, Flavobacterium, Micrococcus, Morganella, Nocardia, Planococcus, Proteus, Propionibacterium, Pseudomonas, Rhodococcus, Sporosarcina, Staphylococcus, Vibrio, Actinomadura, Actinomyces, Kitasatosporia, Streptomyces, Aeromonas, Aureobacterium, Bacillus, Escherichia, Microbacterium, Serratia, Salmonella or Xanthomonas. (III) is a microorganism of the genus Gluconobacter, Acetobacter or Frateuria.
ABEX UPTX: 20001001
EXAMPLE - A 1.2 kilobase XDH **DNA** fragment was amplified from Morganella morganii genomic **DNA**, digested with EcoRI and BamHI, and ligated into EcoRI/BamHI-digested pUC18. The product was used to transform Escherichia coli JM109. The transformants were cultured overnight in L medium (1 percent tryptone, 0.5 percent **yeast** extract, 0.5 percent sodium chloride). The cultures were sonicated and the supernatants (100 microliters) were incubated at 30 degrees Centigrade for 1 minute in a reaction mixture (1 milliliter) containing 100 milliMolar glycine buffer (pH 9.5), 100 milliMolar xylitol and 2 milliMolar nicotinamide adenine **dinucleotide.** One transformant had an **xylitol dehydrogenase** activity of 3.9 Units/milligram (1 unit being the activity required for oxidizing 1 micromole of xylitol to generate 1 micromole of NADH per minute).

L66 ANSWER 6 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **1997-558974** [51] WPIX
DNC **C1997-178545**
TI **Yeast** which ferments xylose to ethanol - comprising xylitol reductase, **xylitol dehydrogenase** and **xylulokinase genes** integrated at each of its multiple reiterated ribosomal **DNA** sites.

DC D16 D17 E17 H06
IN **CHEN, Z; HO, N W Y**
PA (PURD) PURDUE RES FOUND
CYC 76
PI WO 9742307 A1 19971113 (199751)* EN 66p C12N001-16
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN YU
AU 9728301 A 19971126 (199813) C12N001-16
EP 898616 A1 19990303 (199913) EN C12N001-16
R: AT BE DE DK ES FI FR GB GR IE IT NL PT SE
CN 1225125 A 19990804 (199949) C12N001-16
JP 2000509988 W 20000808 (200043) 50p C12N015-09
MX 9809223 A1 19990701 (200061) C12N001-16
AU 731102 B 20010322 (200122) C12N001-16
BR 9710963 A 20010731 (200146) C12N001-16
ADT WO 9742307 A1 WO 1997-US7663 19970506; AU 9728301 A AU 1997-28301 19970506; EP 898616 A1 EP 1997-922698 19970506, WO 1997-US7663 19970506; CN 1225125 A CN 1997-196195 19970506; JP 2000509988 W JP 1997-540153 19970506, WO 1997-US7663 19970506; MX 9809223 A1 MX 1998-9223 19981105; AU 731102 B AU 1997-28301 19970506; BR 9710963 A BR 1997-10963 19970506, WO 1997-US7663 19970506
FDT AU 9728301 A Based on WO 9742307; EP 898616 A1 Based on WO 9742307; JP 2000509988 W Based on WO 9742307; AU 731102 B Previous Publ. AU 9728301, Based on WO 9742307; BR 9710963 A Based on WO 9742307
PRAI US 1996-16865P 19960506
REP 6.Jnl.Ref; WO 9513362
IC ICM C12N001-16; C12N015-09
ICS C12N001-18; C12N001-19; C12N015-68; C12N015-69; C12N015-81; C12P007-06
ICI C12N001-19; C12N001-19; C12N001-19; C12R001:72; C12R001:84; C12R001:85
AB WO 9742307 A UPAB: 19991020
Novel **yeast** which ferments xylose to ethanol, comprises: (a) **xylose reductase** (XR), **xylitol dehydrogenase** (XD) and **xylulokinase** (XK) **genes** integrated at each of its multiple reiterated ribosomal **DNA** sites; (b) multiple copies of exogenous **DNA**, including XR, XD, and XK **genes**, fused to non-glucose inhibited promoters integrated into its **chromosomal DNA**, where the **yeast** simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced **DNA** containing XR, XD and XK **genes**, where the **yeast** ferments xylose to ethanol, where the **yeasts** of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations.
USE - The methods can produce **yeast**, which even upon culture in non-selective medium for multiple generations, e.g. up to 20, retain their full capability to ferment xylose to ethanol.
Dwg.0/12
FS CPI
FA AB; DCN
MC CPI: D05-B03; **D05-H12E**; **D05-H14A2**; D06-G; E10-E04E2; H06-B

L66 ANSWER 7 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **1995-194082** [25] WPIX
DNC **C1995-089834**
TI Recombinant **yeast** encoding **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase** - can effectively ferment xylose alone, or simultaneously with glucose, to produce ethanol e.g. for use as a fuel.

DC D16 E17 H06
IN **HO, N W Y**; TSAO, G T
PA (PURD) PURDUE RES FOUND
CYC 59
PI WO 9513362 A1 19950518 (199525)* EN 63p C12N001-14
RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ
W: AM AU BB BG BR BY CA CN CZ EE FI GE HU JP KG KP KR KZ LK LR LT LV
MD MG MN NO NZ PL RO RU SI SK TJ TT UA UZ VN
AU 9510517 A 19950529 (199537) C12N001-14
EP 728192 A1 19960828 (199639) EN C12N001-14
R: AT BE DE DK ES FR GB GR IE IT NL SE
FI 9601926 A 19960704 (199641) C12N000-00
BR 9408010 A 19961217 (199705) C12N001-14
JP 09505469 W 19970603 (199732) 56p C12N015-09
US 5789210 A 19980804 (199838) C12P007-08
AU 695930 B 19980827 (199846) C12N001-14
CN 1141057 A 19970122 (200047) C12N001-14
ADT WO 9513362 A1 WO 1994-US12861 19941108; AU 9510517 A AU 1995-10517 19941108; EP 728192 A1 WO 1994-US12861 19941108, EP 1995-901176 19941108; FI 9601926 A WO 1994-US12861 19941108, FI 1996-1926 19960507; BR 9408010 A BR 1994-8010 19941108, WO 1994-US12861 19941108; JP 09505469 W WO 1994-US12861 19941108, JP 1995-513948 19941108; US 5789210 A US 1993-148581 19931108; AU 695930 B AU 1995-10517 19941108; CN 1141057 A CN 1994-194767 19941108
FDT AU 9510517 A Based on WO 9513362; EP 728192 A1 Based on WO 9513362; BR 9408010 A Based on WO 9513362; JP 09505469 W Based on WO 9513362; AU 695930 B Previous Publ. AU 9510517, Based on WO 9513362
PRAI US 1993-148581 19931108
REP 4.Jnl.Ref
IC ICM C12N000-00; C12N001-14; C12N015-09; C12P007-08
ICS C07H021-04; C12N001-19; C12N009-00; C12N009-02; C12N009-12; C12N015-00; C12N015-81; C12P007-06
ICI C12N015-09, C12R001:865; C12N001-19, C12R001:865; C12P007-06, C12R001:865
AB WO 9513362 A UPAB: 19951128
Recombinant **yeast** (pref. of the genus **Saccharomyces**) contains introduced **genes** (pref. fused to non-glucose-inhibited promoters) encoding **xylose reductase**, **xylitol dehydrogenase** (XD) and **xylulokinase** effective for fermenting xylose to ethanol. Also claimed are: (1) a recombinant **DNA** molecule comprising **genes** encoding **xylose reductase**, XD and **xylulokinase**; and (2) a vector for transforming **yeast** comprising these **genes.**

USE - The **yeast** can effectively ferment xylose, alone or simultaneously with glucose, to produce ethanol; the ethanol can be used as liquid fuel for cars either as a neat fuel (100% ethanol) or as a blend with petroleum.

ADVANTAGE - The recombinant **yeast** are suitable for ethanol fuel production by fermentation using plant biomass as feedstock.

Dwg.0/14
FS CPI
FA AB; GI; DCN
MC CPI: D05-B03; **D05-H12C**; **D05-H12E**; **D05-H14A2**; D06-B; E10-E04E2; E11-N; H06-B

L66 ANSWER 8 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **1994-167479** [20] WPIX
CR 2001-465360 [50]; 2003-777185 [73]
DNC **C1994-076813**
TI Production of xylitol from recombinant hosts - using a metabolic pathway which uses a carbon source other than D-xylose, D-xylulose or their oligomers.
DC B05 D13 D16 E17
IN APAJALAHTI, J H A; HARKKI, A M; MYASNIKOV, A N; PASTINEN, O A; APAJALAHTI, J; HARKKI, A; MYASNIKOV, A; PASTINEN, O; APAJALAHTI, J H; MJASNIKOV, A N;

NOVOMIROVICH, A; ANDREI, N M
PA (XYRO-N) XYROFIN OY
CYC 47
PI WO 9410325 A1 19940511 (199420)* EN 90p C12P007-18
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL OA PT SE
W: AT AU BB BG BR BY CA CH CZ DE DK ES FI GB HU JP KP KR KZ LK LU LV MG MN MW NL NO NZ PL PT RO RU SD SE SK UA US UZ VN
AU 9454215 A 19940524 (199434) C12P007-18
NO 9501747 A 19950705 (199538) C12P007-18
FI 9502148 A 19950704 (199540) C12N000-00
EP 672161 A1 19950920 (199542) EN C12P007-18
R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE
NZ 257561 A 19960925 (199644) C12P007-18
JP 08505522 W 19960618 (199648) 88p C12N015-09
US 5631150 A 19970520 (199726) 34p C12P019-02
HU 72187 T 19960328 (199741) C12P007-18
EP 672161 B1 19990922 (199943) EN C12P007-18
R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE
DE 69326559 E 19991028 (199951) C12P007-18
BR 9307391 A 19990831 (200002) C12P007-18
ES 2139024 T3 20000201 (200013) C12P007-18
RU 2142999 C1 19991220 (200043) C12N015-52
HU 219016 B 20010131 (200112) C12P007-18
FI 108300 B1 20011231 (200214) C12P007-18
JP 3433295 B2 20030804 (200354) 39p C12N015-09
ADT WO 9410325 A1 WO 1993-FI450 19931105; AU 9454215 A WO 1993-FI450 19931105, AU 1994-54215 19931105; NO 9501747 A WO 1993-FI450 19931105, NO 1995-1747 19950504; FI 9502148 A WO 1993-FI450 19931105, FI 1995-2148 19950504; EP 672161 A1 EP 1993-924615 19931105, WO 1993-FI450 19931105; NZ 257561 A NZ 1993-257561 19931105, WO 1993-FI450 19931105; JP 08505522 W WO 1993-FI450 19931105, JP 1994-510748 19931105; US 5631150 A CIP of US 1992-973325 19921105, Cont of US 1993-110672 19930824, US 1995-368395 19950103; HU 72187 T WO 1993-FI450 19931105, HU 1995-1288 19931105; EP 672161 B1 EP 1993-924615 19931105, WO 1993-FI450 19931105; DE 69326559 E DE 1993-626559 19931105, EP 1993-924615 19931105, WO 1993-FI450 19931105; BR 9307391 A BR 1993-7391 19931105, WO 1993-FI450 19931105; ES 2139024 T3 EP 1993-924615 19931105; RU 2142999 C1 WO 1993-FI450 19931105, RU 1995-113172 19931105; HU 219016 B WO 1993-FI450 19931105, HU 1995-1288 19931105; FI 108300 B1 WO 1993-FI450 19931105, FI 1995-2148 19950504; JP 3433295 B2 WO 1993-FI450 19931105, JP 1994-510748 19931105
FDT AU 9454215 A Based on WO 9410325; EP 672161 A1 Based on WO 9410325; NZ 257561 A Based on WO 9410325; JP 08505522 W Based on WO 9410325; HU 72187 T Based on WO 9410325; EP 672161 B1 Based on WO 9410325; DE 69326559 E Based on EP 672161, Based on WO 9410325; BR 9307391 A Based on WO 9410325; ES 2139024 T3 Based on EP 672161; RU 2142999 C1 Based on WO 9410325; HU 219016 B Previous Publ. HU 72187, Based on WO 9410325; FI 108300 B1 Previous Publ. FI 9502148; JP 3433295 B2 Previous Publ. JP 08505522, Based on WO 9410325
PRAI US 1992-973325 19921105; US 1993-110672 19930824; US 1995-368395 19950103
REP 01Jnl.Ref; EP 450430; WO 9115588
IC ICM C12N000-00; C12N015-09; C12N015-52; C12P007-18; C12P019-02
ICS C12N001-15; C12N001-19; C12N005-10; C12P019-00
AB WO 9410325 A UPAB: 20031112
Production of xylitol from a recombinant host comprises (a) constructing within a microbial host, a novel metabolic pathway leading to the synthesis of xylitol as an end prod. from a carbon source other than D-xylose, D-xylulose or polymers or oligomers containing D-xylose or D-xylulose as major components, (b) growing the recombinant host under conditions that provide for the synthesis of the xylitol using the pathway and on a carbon source other than those in (a), and (c) recovering the xylitol. Pref. the recombinant host may be transformed with a construct-encoding enzymes such as D-glucose-6-phosphate dehydrogenase

(GPD), 6-phospho-D-gluconate dehydrogenase (PGD), D-ribulose-5-phosphate-3-epimerase (RPE), D-ribulokinase (RK), **xylitol dehydrogenase** (XD) and D-arabitol dehydrogenase (AD).

USE/ADVANTAGE - The xylitol produced is used as a sweetener. The method can be used to produce xylitol using readily available sources such as D-glucose.

Dwg.0/0

FS CPI

FA AB; DCN

MC CPI: B04-F09; B10-E04C; B11-A01; B14-E11; D03-H01A; D05-C08; **D05-H14A**; **D05-H17A3**; E10-A07

ABEQ US 5631150 A UPAB: 19970626

A method for production of xylitol from a recombinant microbial host, comprises:

a) growing an arabitol-producing **yeast** or an arabitol-producing fungus under conditions that provide for the synthesis of xylitol, where the arabitol-producing **yeast** or arabitol-producing fungus has been modified to synthesize xylitol as an end product in a fermentation when grown on D-arabitol or a carbon source that the unmodified arabitol-producing **yeast** or unmodified arabitol-producing fungus utilized for D-arabitol biosynthesis, the carbon source being other than D-xylose, D-xylulose, mixtures of D-xylose and D-xylulose, and polymers and oligomers containing D-xylose or D-xylulose as major components under conditions that provide for synthesis of xylitol where before the modification the host produced D-arabitol but did not utilize D-arabitol for the synthesis of xylitol, and the host has been transformed with a **DNA** encoding a D-xylulose forming D-arabitol dehydrogenase (E.C. 1.1.1.11) and with a **DNA** encoding **xylitol dehydrogenase** (E.C. 1.1.1.9); and

b) recovering the xylitol produced in step a.

Dwg.0/11

L66 ANSWER 9 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN **1991-325230** [44] WPIX

DNC **C1991-140554**

TI **DNA** encoding **xylose reductase** and/or **xylitol dehydrogenase** - useful for transforming **yeast** strains for expression of one enzyme or co-expression of both.

DC B05 D13 D16 E17 F09

IN AIRAKSINEN, U; HAHN-HAGERDAL, B; HALLBORN, J; KERANEN, S; OJAMO, H; PENTTILA, M; WALFRIDSSON, M; HAHN-HAEGERDAL, B; KERAENEN, S; PENTTILAE, M; HAHNHAGERD, B; WALFRIDSSO, M

PA (VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS; (XYRO-N) XYROFIN OY; (VALW) VALTION TEKNILLINEN; (HALL-I) HALLBORN J

CYC 20

PI	WO 9115588	A	19911017 (199144)*	47p		
	RW: AT BE CH DE DK ES FR GB GR IT LU NL SE					
	W: AU CA FI JP NO US					
	AU 9175657	A	19911030 (199205)			
	FI 9204461	A	19921002 (199302)			C12N000-00
	NO 9203880	A	19921006 (199306)			C12N015-53
	EP 527758	A1	19930224 (199308)	EN		C12N015-53
	R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE					
	JP 05507843	W	19931111 (199350)		17p	C12N015-53
	AU 647104	B	19940317 (199416)			C12N015-53
	EP 527758	B1	19980107 (199806)	EN	24p	C12N015-53
	R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE					
	DE 69128619	E	19980212 (199812)			C12N015-53
	ES 2113373	T3	19980501 (199824)			C12N015-53
	US 5866382	A	19990202 (199912)			C12P007-02
	FI 9902153	A	19991006 (200003)			C12N000-00
	FI 104636	B1	20000315 (200020)			C12N015-53

```
     NO 308544     B1 20000925 (200056)              C12N015-53
     CA 2090122    C  20020618 (200250)  EN          C12N015-53
     JP 3348215    B2 20021120 (200282)       21p    C12P007-18
     US 6582944    B1 20030624 (200343)              C12P007-06
     FI 112250     B1 20031114 (200377)              C12P007-06
ADT  FI 9204461 A WO 1991-FI103 19910408, FI 1992-4461 19921002; NO 9203880 A
     WO 1991-FI103 19910408, NO 1992-3880 19921006; EP 527758 A1 EP 1991-906996
     19910408, WO 1991-FI103 19910408; JP 05507843 W JP 1991-506907 19910408,
     WO 1991-FI103 19910408; AU 647104 B AU 1991-75657 19910408; EP 527758 B1
     EP 1991-906996 19910408, WO 1991-FI103 19910408; DE 69128619 E DE
     1991-628619 19910408, EP 1991-906996 19910408, WO 1991-FI103 19910408; ES
     2113373 T3 EP 1991-906996 19910408; US 5866382 A CIP of US 1990-527775
     19900524, Cont of US 1992-848694 19920309, US 1994-336198 19941103; FI
     9902153 A WO 1991-FI103 19910408, Div ex FI 1992-4461 19921002, FI
     1999-2153 19991006; FI 104636 B1 WO 1991-FI103 19910408, FI 1992-4461
     19921002; NO 308544 B1 WO 1991-FI103 19910408, NO 1992-3880 19921006; CA
     2090122 C CA 1991-2090122 19910408, WO 1991-FI103 19910408; JP 3348215 B2
     JP 1991-506907 19910408, WO 1991-FI103 19910408; US 6582944 B1 CIP of US
     1990-527775 19900524, CIP of WO 1991-FI103 19910408, Cont of US
     1992-848694 19920309, Div ex US 1994-336198 19941103, US 1999-184965
     19990108; FI 112250 B1 WO 1991-FI103 19910408, Div ex FI 1992-4461
     19921002, FI 1999-2153 19991006
FDT  EP 527758 A1 Based on WO 9115588; JP 05507843 W Based on WO 9115588; AU
     647104 B Previous Publ. AU 9175657, Based on WO 9115588; EP 527758 B1
     Based on WO 9115588; DE 69128619 E Based on EP 527758, Based on WO
     9115588; ES 2113373 T3 Based on EP 527758; FI 104636 B1 Previous Publ. FI
     9204461; NO 308544 B1 Previous Publ. NO 9203880; CA 2090122 C Based on WO
     9115588; JP 3348215 B2 Previous Publ. JP 05507843, Based on WO 9115588; US
     6582944 B1 Div ex US 5866382; FI 112250 B1 Previous Publ. FI 9902153
PRAI FI 1990-1771     19900406
REP  7.Jnl.Ref
IC   ICM  C12N000-00; C12N015-53; C12P007-02; C12P007-06; C12P007-18
     ICS  C07H021-04; C12N001-15; C12N001-19; C12N009-02; C12N015-52;
          C12N015-81; C12P019-02
ICA  C12N009-04; C12N015-09
ICI  C12P007-18, C12R001:865
AB   WO   9115588 A UPAB: 20040123
       DNA (I) encoding xylose reductase enzyme (A)
     is new. When (I) is transferred into a yeast strain it renders
     the strain capable of reducing xylose to xylitol.
          Pref. the yeast of (1) is capable of integrating to the
     yeast chromosome when transformed into a yeast
     strain. (I) and/or (II) is expressed under yeast gene
     regulatory regions, e.g. promoters of (A), (B), yeast alcohol
     dehydrogenase gene ADH1 or yeast phosphoglycerate
     kinase gene PGK1, and functional fragments. The yeast
     strain is a Saccharomyces cerevisiae strain (pref.),
     kluyveromyces strain, Schizosacchoromyces pombe strain or Pichia strain.
          The yeast vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60
     and pJHXDH70, and the yeast strains. S. cerivisiae H475, H477,
     H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are
     specifically claimed.
          USE - The yeast transformants can reduce xylase to xylitol
     for use by diabetics or as a natural sweetener. The co-expression of the
     two enzymes in a yeast strain results in the production of ethanol.
     Dwg.0/8
FS   CPI
FA   AB; DCN
MC   CPI: B04-B02B2; B04-B02C2; B04-B04A1; B10-A07; B10-E04D; B11-A; B12-J01;
          B12-L03; D05-B03; D05-C03B; D05-C03D; D05-H03B;
          D05-H12; E10-A07; F05-A02C; F05-B
ABEQ EP    527758 A UPAB: 19930928
       DNA (I) encoding xylose reductase enzyme (A)
```

is new. When (I) is transferred into a **yeast** strain it renders the strain capable of reducing xylose to xylitol.

Pref. the **yeast** of (1) is capable of integrating to the **yeast chromosome** when transformed into a **yeast** strain. (I) and/or (II) is expressed under **yeast gene** regulatory regions, e.g. promoters of (A), (B), **yeast** alcohol dehydrogenase **gene** ADH1 or **yeast** phosphoglycerate kinase **gene** PGK1, and functional fragments. The **yeast** strain is a **Saccharomyces** cerevisiae strain (pref.), kluyveromyces strain, Schizosaccharomyces pombe strain or Pichia strain.

The **yeast** vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60, and pJHXDH70, and the **yeast** strains S. cerivisiae H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.

USE - The **yeast** transformants can reduce xylase to xylitol for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a **yeast** strain results in the prodn. of ethanol

ABEQ EP 527758 B UPAB: 19980209

DNA (I) encoding **xylose reductase** enzyme (A) is new. When (I) is transferred into a **yeast** strain it renders the strain capable of reducing xylose to xylitol.

Pref. the **yeast** of (1) is capable of integrating to the **yeast chromosome** when transformed into a **yeast** strain. (I) and/or (II) is expressed under **yeast gene** regulatory regions, e.g. promoters of (A), (B), **yeast** alcohol dehydrogenase **gene** ADH1 or **yeast** phosphogylcerate kinase **gene** PGK1, and functional fragments. The **yeast** strain is a **Saccharomyces** cerevisiae strain (pref.), kluyveromyces strain, Schizosacchoromyces pombe strain or Pichia strain.

The **yeast** vectors pUA103, pUA107, pJHXR22, pMW22, pJHXDH60 and pJHXDH70, and the **yeast** strains. S. cerivisiae H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.

USE - The **yeast** transformants can reduce xylase to xylitol for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a **yeast** strain results in the prodn. of ethanol.

Dwg.0/8

L66 ANSWER 10 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **1991-296506** [41] WPIX
DNC **C1991-128227**
TI New **DNA** encoding **xylose reductase** and **xylitol dehydrogenase** - and transformed **yeast** for production of ethanol and biomass from xylose or recovery of oxidised NADP.
DC B02 B04 D16 E17
IN AMORE, R; HAGEDORN, J; HOLLENBERG, C P; KOTTER, P; PIONTEK, M; STRASSER, A W M; VONCIRIACY, M; KOETTER, P; VON, CIRIACY-WANTRUP M; HAGENDORN, J
PA (RHEI-N) RHEIN BIOTECH NEUE BIOTECHNOLOGISCHE PROZESSE & PROD GMBH; (RHEI-N) RHEIN BIOTECH GES NEUE BIOTECHNOLOGISCHE; (RHEI-N) RHEIN BIOTECH GES B; (RHEI-N) RHEIN BIOTECH GMBH
CYC 16
PI

DE 4009676	A	19911002 (199141)*		50p	
EP 450430	A	19911009 (199141)		50p	
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE					
CA 2039021	A	19910927 (199150)			
EP 450430	A3	19920102 (199320)		50p	
DE 4009676	C2	19930909 (199336)		51p	C12N001-19
JP 06339383	A	19941213 (199509)		32p	C12N015-53
EP 450430	B1	19970625 (199730)	EN		C12N015-53
R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE					
DE 69126632	E	19970731 (199736)			C12N015-53
ES 2104626	T3	19971016 (199748)			C12N015-53

JP 2000139486 A 20000523 (200033) 21p C12N015-09
JP 3122153 B2 20010109 (200104) 32p C12N015-09
JP 2001103988 A 20010417 (200128) 27p C12N015-09
JP 3193917 B2 20010730 (200146) 27p C12N015-09

ADT DE 4009676 A DE 1990-4009676 19900326; EP 450430 A EP 1991-104558 19910322; EP 450430 A3 EP 1991-104558 19910322; DE 4009676 C2 DE 1990-4009676 19900326; JP 06339383 A JP 1991-62160 19910326; EP 450430 B1 EP 1991-104558 19910322; DE 69126632 E DE 1991-626632 19910322, EP 1991-104558 19910322; ES 2104626 T3 EP 1991-104558 19910322; JP 2000139486 A Div ex JP 1991-62160 19910326, JP 2000-589 19910326; JP 3122153 B2 JP 1991-62160 19910326; JP 2001103988 A Div ex JP 1991-62160 19910326, JP 2000-276227 19910326; JP 3193917 B2 Div ex JP 1991-62160 19910326, JP 2000-276227 19910326

FDT DE 69126632 E Based on EP 450430; ES 2104626 T3 Based on EP 450430; JP 3122153 B2 Previous Publ. JP 06339383; JP 3193917 B2 Previous Publ. JP 2001103988

PRAI DE 1990-4009676 19900326

REP NoSR.Pub; 6.Jnl.Ref; EP 238023; GB 2151635; JP 60199383; JP 61063291; US 4840903

IC C07H021-04; C07K015-04; C12C011-00; C12N001-19; C12N009-02; C12N015-63; C12P007-06; C12P019-34

ICM C12N001-19; C12N015-09; C12N015-53

ICS C07H021-04; C07K013-00; C07K015-04; C12C011-00; C12N001-14; C12N001-21; C12N009-02; C12N009-04; C12N015-63; C12N015-81; C12P007-06; C12P007-10; C12P019-34; C12P021-02

ICI C12N009-02; C12N009-02; C12N015-09; C12N015-09; C12N015-09; C12R001:645; C12R001:84; C12R001:84; C12R001:85; C12R001:865; C12N001-19; C12N001-19; C12N001-19; C12N001-21; C12N009-04; C12N015-09; C12P007-06; C12P007-06; C12P007-06; C12P007-06; C12R001:01; C12R001:01; C12R001:645; C12R001:645; C12R001:84; C12R001:84; C12R001:84; C12R001:84; C12R001:865; C12R001:865; C12N001-19, C12R001:865; C12N009-02, C12R001:865; C12P007-06, C12R001:865; C12N015-53, C12R001:645; C12N001-19, C12R001:865; C12N009-02, C12R001:865

AB DE 4009676 A UPAB: 19971030

New **DNA** sequence (I) comprises a structural **gene** encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

Also new are (1) combinations of (I) with other **DNA** halogen sequences for regulating expression; (2) vectors and microorganisms containing (I), and (3) XR and XDH produced by expressing (I).

More specifically, (I) is derived from a **yeast**, specifically Pichia stipitis CBS 5773 (DSM 5855). The specification includes sequences for **DNA** fragments which encode XR (2040 bases) and XDH (1950 bases), and the derived structures (318 and 363 amino acids, respectively).

USE/ADVANTAGE - XR and XDH are useful (1) for production of ethanol from xylose (a waste prod. of cellulose mfr.); (2) for production of biomass and (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with (I) can ferment highly concentrate carbohydrate solns. prior art and are tolerant to EtOH, pH and temperature. Also contemplated is production of specific proteins (II) in P. stipitis by expressing the structural **gene** for (II) under control of the 5'-regulatory region of the XR and XDH **genes** of P. stipitis (these are inducible by xylose) and/or the ADH1 promoter of S. cerevisiae and/or the glucoamylase promoter of Schwanniomyces occidentalis. P. Stipitis has an efficient secretory system and can use xylose as a C source. @(50pp Dwg.No.0/7)

FS CPI

FA AB; DCN

MC CPI: B04-B02B2; B04-B02C2; B04-B04A1; D05-C03B; **D05-H03B**; **D05-H05**; **D05-H12**; E10-E04E2

ABEQ EP 450430 A UPAB: 19931113
New **DNA** sequence (I) comprises a structural **gene** encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.
Also new are (1) combinations of (I) with other **DNA** halogen sequences for regulating expression; (2) vectors and microorganisms contg. (I), and (3) XR and XDH produced by expressing (I).
More specifically, (I) is derived from a **yeast**, specifically Pichia stipitis CBS 5773 (DSM 5855). The specification includes sequences for **DNA** fragments which encode XR (2040 bases) and XDH (1950 bases), and the derived structures (318 and 363 amino acids, respectively).
USE/ADVANTAGE - XR and XDH are useful (1) for prodn. of ethanol from xylose (a waste prod. of cellulose mfr.); (2) for prodn. of biomass and (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with (I) can ferment highly conc. carbohydrate solns. prior art and are tolerant to EtOH, pH and temp.. Also contemplated is prodn. of specific proteins (II) in P. stipitis by expressing the structural **gene** for (II) under control of the 5'-regulatory region of the XR and XDH **genes** of P. stipitis (these are inducible by xylose) and/or the ADH1 promoter of S. cerevisiae and/or the glucoamylase promoter of Schwanniomyces occidentalis. P. Stipitis has an efficient secretory system and can use xylose as a C source. @(50pp Dwg.No.0/7)

ABEQ DE 4009676 C UPAB: 19931122
Recombinant **DNA** sequence that encodes the prodn. of an xylosereductase and/or xylitoldehydrogenase has been utlised in expression vectors contg. this **DNA** to produce the enzymes. Host cells have been transformed with these vectors and then propagated to produce the exogenous polypeptides. The **nucleotide** sequence of the **cDNA** and the aminoacid sequences of the polypeptides are defined.
USE - The prods. facilitate the degradation of xylose from wood pulp, leading to the conversion of waste biomass to alcohol.
Dwg.0/7

ABEQ EP 450430 B UPAB: 19970723
New **DNA** sequence (I) comprises a structural **gene** encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

L66 ANSWER 11 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN
AN **1990-276784** [37] WPIX
DNN **N1990-213906** DNC **C1990-119559**
TI **DNA** coding for placenta-specific protein-9 - and recombinant protein with **aldose reductase** activity.
DC B04 D16 P34 S03
IN GRUNDMANN, U; AMANN, E
PA (BEHW) BEHRINGWERKE AG
CYC 18
PI EP 386733 A 19900912 (199037)*
R: AT BE CH DE ES FR GB IT LI LU NL SE
DE 3907744 A 19900920 (199039)
AU 9051103 A 19900913 (199044)
PT 93381 A 19901107 (199047)
CA 2011877 A 19900910 (199048)
JP 02295486 A 19901206 (199104)
EP 386733 B1 19950705 (199531) DE 11p C12N015-12
R: AT BE CH DE DK ES FR GB IT LI LU NL SE
DE 59009360 G 19950810 (199537) C12N015-12
ES 2076238 T3 19951101 (199550) C12N015-12
IE 67797 B 19960501 (199629) C12N015-12
ADT EP 386733 A EP 1990-104352 19900307; DE 3907744 A DE 1989-3907744 19890310; JP 02295486 A JP 1990-59800 19900309; EP 386733 B1 EP

1990-104352 19900307; DE 59009360 G DE 1990-509360 19900307, EP 1990-104352 19900307; ES 2076238 T3 EP 1990-104352 19900307; IE 67797 B IE 1990-853 19900309
FDT DE 59009360 G Based on EP 386733; ES 2076238 T3 Based on EP 386733
PRAI DE 1989-3907744 19890310
REP 1.Jnl.Ref; EP 37963; 01Jnl.Ref
IC A61K031-70; A61K037-02; A61N037-02; C07H021-04; C07K013-00; C07K015-12; C07K015-28; C12N001-21; C12N005-00; C12N015-12; C12P021-02; C12Q001-68; G01N033-53; G01N033-68
ICM C12N015-12
ICS A61K031-70; A61K037-02; A61N037-02; C07H021-04; C07K013-00; C07K015-12; C07K015-28; C12N001-21; C12N005-00; C12P021-02; C12Q001-68; G01N033-53; G01N033-577; G01N033-68
ICI C12N001-21, C12R001:
AB EP 386733 A UPAB: 19930928
The following are claimed: (a) **DNA** coding for placenta-specific protein 9 (PP9), where the amino acid sequence of PP9 and the coding sequence of the **DNA** are shown in the fig.; (b) **DNA** and RNA which hybridise with **DNA** (a) under stringent conditions; (c) **gene** structures, vectors and transformed cells containing **nucleic** acids (a) or (b); (d) PP) when produced in E. coli, **yeast** or animal cells by expression of **DNA** (a); (e) polyclonal and monoclonal antibodies specific to PP9, when produced by immunisation with recombinant
USE - PP9 is probably identical to human **aldose reductase** and is thus useful for screening and identifying **aldose reductase** inhibitors for treatment of diabetic complications. The **nucleic** acid and antibodies are useful for diagnostic purposes, and the antibodies are also useful for purificn. of PP9 by affinity chromatography.
1/1
FS CPI EPI GMPI
FA AB; GI
MC CPI: B04-B02B1; B04-B02B2; B04-B02C2; B04-B04A; B04-B04C5; B04-B04C6; B12-H05; **D05-H09**; **D05-H11**; **D05-H12**
EPI: S03-E14H
ABEQ EP 386733 B UPAB: 19950810
A **nucleotide** sequence shown in Table 1, or a sequence derived therefrom on the basis of the degeneracy of the **genetic** code, coding for placenta-specific protein PP9.
Dwg.0/1

=> d his

(FILE 'HOME' ENTERED AT 15:35:08 ON 04 MAR 2004)

FILE 'REGISTRY' ENTERED AT 15:35:42 ON 04 MAR 2004
SET COST OFF
E XYLOSE REDUCTASE/CN
L1 4 S E3
E XYLITOL DEHYDROGENASE/CN
L2 2 S E3
E XYLULOKINASE/CN
L3 1 S E3
L4 26 S XYLOSE REDUCTASE
L5 7 S XYLITOL DEHYDROGENASE
L6 33 S XYLULOKINASE

FILE 'HCAPLUS' ENTERED AT 15:37:10 ON 04 MAR 2004
L7 2967 S L1-L6
L8 464 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE
L9 3153 S ALDOSE REDUCTASE

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L10          68 S XYLULOSE REDUCTASE
L11          50 S XYLULOSE KINASE
L12        3760 S L7-L11
L13         218 S L12 AND YEAST
               E YEAST/CT
L14          25 S L12 AND E3-E53
               E E53+ALL
L15       12225 S E1
               E E2+ALL
L16       34588 S E6,E5+NT
L17          25 S  L12 AND L15,L16
L18         218 S L13,L14,L17
L19           1 S YEAST(L)1400(L)LNH(L)ST
               E SACCHAROMYCES/CT
L20           9 S L12 AND E3
L21         114 S L12 AND E3-E196
               E E3+ALL
L22           0 S L12 AND E4
L23         113 S L12 AND E5+NT
L24         269 S L18,L20-L23
L25          32 S L24 AND DNA
L26          31 S L24 AND PLASMID
L27          20 S L24 AND CHROMOSOM?
L28         126 S L24 AND GENE
L29          74 S L24 AND GENETIC?/SC,SX
L30         130 S L25-L29
L31         269 S L24-L30
               E WO97-US7663/AP,PRN
L32           1 S E3,E4
               E US96-016865/AP,PRN
L33           1 S E5
               E HO N/AU
L34          20 S E3,E11,E12
L35          36 S E28,E31,E32
               E CHEN Z/AU
L36         722 S E3,E7
               E CHEN ZHENG/AU
L37         261 S E3,E4
L38           8 S E51
L39           1 S L31 AND L32,L33
L40          11 S L31 AND L34-L38
L41          11 S L32,L33,L39,L40
L42         134 S L31 AND (PD<=19960506 OR PRD<=19960506 OR AD<=19960506)
L43           9 S L41 AND L42
L44          11 S L41,L43
L45          27 S L42 AND GENETIC?/SC,SX
L46          31 S L44,L45
L47         105 S L42 NOT L46
               SEL DN AN 22 34 L47
L48           2 S E1-E6 AND L47
L49          33 S L46,L48 AND L7-L48
               SEL HIT RN

     FILE 'REGISTRY' ENTERED AT 16:16:43 ON 04 MAR 2004
L50          14 S E7-E20
L51          14 S L50 AND L1-L6

     FILE 'REGISTRY' ENTERED AT 16:17:14 ON 04 MAR 2004

     FILE 'HCAPLUS' ENTERED AT 16:17:29 ON 04 MAR 2004

     FILE 'WPIX' ENTERED AT 16:17:48 ON 04 MAR 2004
L52         784 S L8/BIX OR L9/BIX OR L10/BIX
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L53          24 S L52 AND YEAST/BIX
L54           0 S L19/BIX
L55          11 S L52 AND SACCHAROMYC?/BIX
L56          21 S L52 AND (?PLASMID? OR ?CHROMOSOM?)/BIX
L57          38 S L53,L55,L56
L58           2 S L52 AND (HO N? OR CHEN Z?)/AU
L59           2 S L57 AND L58
L60          27 S L57 AND D05-H?/MC
L61          30 S L57 AND (GENE OR GENETIC? OR DNA OR CDNA)/BIX
L62          15 S L57 AND (?NUCLEIC? OR ?NUCLEO?)/BIX
L63          32 S L59-L62
L64           6 S L57 NOT L63
               SEL DN AN 5 15-17 20 25 27-31 L63
L65          11 S E21-E43 AND L63
L66          11 S L59,L65

     FILE 'WPIX' ENTERED AT 16:25:58 ON 04 MAR 2004

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